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VERFION KEYWORDS SOURCE

OFGANISM

Homo sapiens

human.

Eukaryėta; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Primates; Caturrhini; Hominidae; Homo.

ACCE-TON

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H.sapiers mRNA for 708768 91877211 908768.1 GI:187721: 1L-13 receptor.

GI:1877211

RESULT ESILIS LOCUS

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mRNA receptor.

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Q: 1382 aacacctacccaaaaatgattccagaatttttctgtgatacatgaagaagattttgcatct	1077 GATGACGGAATTTGG 1262 gtgaagacctatcgaagaaaac		Oy 782 ggagcagtgaggcatcagactataaagatttctatatttgtgttaatggatcatcagaga	Db 492 Q7 542 9tt Q7 543 GTT Q9 602 tgt D5 588 TGT C9 662 act C9 662 act C9 722 tga Db 680 TGA

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18 21	acaagettttgeaetteatetteayacacegagataaaagttaaceeteeteaggatttt	Qy 122 Db 169
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	IL-13 cytokine recepto Patent: US 5710023-A 3 Location/Qual 1, 1369	TITLE JOURNAL FEATURES
<u>α</u>	Unknown.  SM Unknown.  Unclassified.  1 (bases 1 to 1369)  COllins,M., Donaldson,D., Fitz,L., Neben,T., Whitters,M. and Wood C	SOURCE ORGANISM REFERENCE AUTHORS
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                                                                                                                                                                                               atgtctgggtacttcttgataccaattaccaacttgttttactggtatgagggcttggatc
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                                                                                                                                                                                                                                                                                                       atatcaccacaaggaattccagaaactaaagttcaggattaagttttgggtagaatggat 571
                                                                                                                                                                                                                                                                                                                                                         acaaatggatcagaagttcaaagttccaattgctaggagtgggcagaaactacttattgg
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                                                                                                                                                                                   ---AGACAGTATATTCTGATACCAACTATACCATGTTTTTCTGGTATGAGGGCTTGGATC
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Submitted (31-JUL-1996) Molecular Immunology, Genetics Institute,
87 CambridgePark Dr., Cambridge, MA 02140, USA
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Donaldson,D.D., Whitters,M.J., Fitz,L., Neben,T.Y., Finnerty; Belederson,S.L., O'Hara,R.M. Jr., Beler,D.R., Turner,K.J., Wooned Collins, E.J., Whitter, M.J., Beler,D.R., Turner, K.J., Wooned Collins, E.J., Whitter, M.J., Whitter
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/product="IL-13 receptor alpha 2"
/product="IL-13 receptor alpha 2"
/protein_id="AAC33240.1"
/db_xref="pID:93483094"
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/franslation="MAFVHIRCLCFILLCTITGYSLEIKYNPFODFEDLMKGIEGKIRTH
LSEHCTINGSEVQSPHIRESYGISDESSLETKIDMKGIFTOMGYLVCSMKFGKTYYSD
INVTMFFWYEGLDHALQCADYLQHDEKNYGCKLSNLDSSDYKDFFICYNGSSKLEPIR
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IIFIVPVCLFFIFLLLLCLIVEKEEPEPTLSLHVDLNKEVCAYEDTLC"
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/dev_stage="8 wk"
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/strain="C3H/HeJ"
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                      ccttgaaaacaacaaatgaaacccgaataatagagtttttagtagcaattatgctttgta 1171
                                                                                                               tttaggcgtggacctattccagcaaggtgttttgattatgaaattgagatcagagaaagat 1051
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 TGAAGAGGAGAGCAAATGAAA - - -
                                                                                                                                                 TTCCTTCATATTAGTGTGGAGAATTCCATTGATATTAGAATGAAATGGAGCACACCT---
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                                                                                                                                                                                                                                                                                                                                                                                                                                      1498 CATGTAGGCATCACTGTAATTACCTATCTATGCAAGTAGTTAAAGAGATAGAAGAATTTG 1439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   source
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          tgataaacaatgctgggaaggtgaagacctatcgaagaaaa 1282
                                                                                                                                                                                                                                                                                                          aacaaatgaaacccgaataatagagtttttagtagcaattatgctttgtagtaagaagca 1181
                                                                                                                                                                                                                                                                                                                                                          aaagcatggaggaattttggtgactgctacagttgaaaatgaaacatacaccttgaaaac 1121
                                                                                                                                                                                                                                                                                                                                                                                                           gacctattccagcaaggtgttttgattatgaaattgagatcagagaagatgatactaccg 1061
                                                                                                                                                                                                                                                                                                                                                                                                                                                          ttactcgggagagttcatgtgaaattaagctgaaatggagcatacctttgtttaggcgtg 1001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    spore germination-specific protein.
Dictyosteliu discoideum (strain AX-3) cDNA
Dictyostelium discoideum
Eukaryota; Dictyosteliida; Dictyostelium.
11 (bases 1028 to 2982)
                                                                                   DDISGSPA 2982 bp
Dictyosteliu discoideum
complete cds
M33862 J02916
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166494:1
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Dorner,F., Scheiflinger,F. and Falkner,
Recombinant fowlpox virus
Patent: US 5670387-A 14 23-SEP-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unknown
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unclassified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   h 3.4%; Score 52.6; DB Similarity 7.0%; Pred. No. 0.051; 28; Conservative 207; Mismatches
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Best Local Similarity
Matches 157; Conserv
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gggatcgtttctggctaccatttggtttcatcttaatattagttatatttgtaaccggtc 1356
                                         AAAAATAAAAAAAAAAAAAAAAAAAAAATATAGGTTTTATTTAAATATTTTCTT
                                                                   tggagtgataaacaatgctgggaaggtgaagacctatcgaagaaaactttgctagtagct 1296
                                                                                                                                                       aagcaaagtgaatatttattgctcagatgacggaatttgggcaaagaatcaagtagtgag 1236
                                                                                                                                                                                                Shaw,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (18-JUL-1995) David R. Shaw,
Biology, 340 Kingsland Street, Nutley,
On Aug 1, 1995 this sequence version re
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Giorda,R., Ohmachi,T., Shaw,D.R. and Ennis,H.L. A shared internal threonine-glutamic acid-threonine-proline repeat defines a family of Dictyostelium discoideum spore germination
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (17-APR-1990) Herbert L. Ennis, Roche Institute of Molecular Biology, 340 Kingsland Street, Nutley, NJ 07110-1150,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ennis, H.L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Biochemistry 29 (31), 7264-7269 (1990)
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                                                                                                                                                                                                                                                                            2.9%;
llarity 45.8%;
Conservative
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SFYTSDGNSHDVKSSDGSVSSSVFSGSLTNPGIFKVTLTKEGNIEFTSSYDEGLSATI
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417 c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GSHTFGYIVKSAELSDLEGVQYTC
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SSTTGNSGTTGSATTTTSSSSDNSDGSVGTSTTTSPAITTSSGSIIDPTSPPTTDSSS
NSGGYGSSSSIENGVECLLTITQDAFDSWTYDNIIYTVYQVNLTNIGTLSVESVILTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /db_xref="PID:g167881"
/db_xref="GI:167881"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'product="cellulose binding protein"
'protein_id="AAA73632.1"
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)oin(1196. .
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84. .1253
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Pred. No. 2.1;
0; Mismatches 186;
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y, NJ 07110-1150, USA
replaced gi:167880.
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                                                                                                                                                                                                                                                                                                                              Baker, J., Baldwin, J., Barna, N., Beckerly, R., Benn, J., Brown, A., Castle, A., Cerny, J., Colangelo, M., Collins, S., Collymore, A., Croke, P., Devar, K., Devar, K., Devar, K., Devar, K., Devar, K., Donelan, L., Doyle, M., Ferreira, P., Fitzhugh, W., Forrest, C., Fuske, R., Gage, D., Galagan, J., Gardyna, S., Gilbert, D., Grant, G., Hagos, B., Heaford, A., Horton, L., Howland, J.C., Jones, C., Kann, L., Karatas, A., Lehoczky, J., Lieu, C., Locke, K., Macdonald, P., Marquis, N., McEwan, P., McGurk, A., McKernan, K., McLaughlin, J., Meljin, J., Molla, M., Morris, W., Morrow, J., Mychalecky, J., Naloff, M., O'Connor, T., O'Donnell, P., Pavlin, B., Peterson, K., Pollara, V., Riley, R., Robert, D., Roy, A., Severy, P., Stange-Thomann, N., Stojanovic, N., Stone, C., Subramanian, A., Tesfaye, S., Torruella-Miller, I., Vassillev, H., Vo, A., Wagner, A., Theeler, J., Wu, X., Wyman, D., Ye, W.J. and Zody, M.
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AC007435
g5578733
                                                                                                                                          Submitted (30-JUL-1999) Whitehead Institute/MIT Center Research, 320 Charles Street, Cambridge, MA 02141, USA On Jul 23, 1999 this sequence version replaced gi:55237
                                                                                               All repeats were identified using
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (29-APR-1999) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
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D.rect Submission
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http://ftp.genome.washington.edu/RM/RepeatMasker.html
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/clone="6_C_10"
rpt_family="(G)n"
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plement(3560 .3850)
_family="AluSg1"
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lement(17078. .17376)
_family="Charlielb"
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_family="L2"
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7. .16749
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_family="AluJo/FRAM"
lement(4898. .5113)
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ement(480"
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. .16289
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12866
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. .11080
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ement(6226. .6
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                                                                                                                         ly="AT_rich"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ly-"LIMEC"
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       Ouery Match 2.9%;
Best Local Similarity 49.2%;
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complement(31015. .31082)
/rpt_family="Looper"
31109. .31298
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(Complement(32713. .33164)
/rpt_family="Looper"
33251. .33330
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18493, .18521
                                                                                              /rpt_family="Looper"
complement/3/30"
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complement(33603. .33823)
/rpt_family="LIMC4"
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complement(18801...19041)
/rpt_family="L2"
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complement(27000 .27228)
/rpt_family="MIR"
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complement(31726. .3
                                                                                                                                      family-"MER45"
                                                                                                                                                                                                                                                                                        _family="Looper"
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5. .26776
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         Score 44.4; DB 41; Length 178342; Pred. No. 1.5; 0; Mismatches 121; Indels 0;
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TITLE
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Best Local Similarity
1400 attccagaatttttctgtgatacatgaagaagatttgcatctttccatatcaagagacat 1459
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                                                                                                                                                                                                                                                                                                                                                          Japan Science and Technology Corporation (JST)
5-3, Yonbancho, Chiyoda-ku, Tokyo 102-0081 Japan
For further infomation about this sequence, including its location
and relationship to other sequences, please visit our sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Fax:81-3-5214-8470)
This sequence is conducted by Japanese Foundation for Cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (30-NOV-1998) to the DDBJ/EMBL/GenBank databases. Mika Hirakawa, Japan Science and Technology Corporation (JST), Advance Database Department; 5-3, Yonban-cho, Chiyoda-ku, Tokyo 102-0028, Japan (E-mail:mika@tokyo.jst.go.jp, Tel:81-3-5214-8491,
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Homo sapiens genomic DNA of 8p21.3-p22 anti-oncogene of
hepatocellular colorectal and non-small cell lung cancer , segment
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Hirakawa,M., Yamaguchi,H., Imai,K. and Shimada,J.
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On Sep 23, 1999 this sequence version replaced gi:4558576.
The Morking draft' sequence. It currently
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tonsists of 16 contigs. The true order of the pieces
to not known and their order in this sequence record is
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Corway,A.B. and Davis,R.W.
clasmodium falciparum 3D7 chromosome 12
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AC004106
Muzny,D., Arenson,A.D., Adams,C., Brundage,E., Bunac,C., Carvelli,K., Chacko,J., Chen,J., Di,W., Ding,Y., Dugan,S.
                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 190482)
                                                                                                                                                                                            AC004106 190482
Homo sapiens Xp22
                                                                                 Homo sapiens
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/db_xref="taxon:5833"
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Pred. No. 1
             Adams, C.,
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FEATURES

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                                                                                       Submitted (22-MAY-1998) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
On May 22, 1998 this sequence version replaced gi:3126769.
Sequencing is completed to a minimum standard of double strand coverage with a minimum of 2 clones and 2 reads with no ambiguities or 2 chemistries with a minimum of 2 clones and 3 reads with no ambiguities. If the sequence quality does not meet this standard, it will be indicated in the annotation.
                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (03-FEB-1998) Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA (bases 1 to 190482)
The repeat regions shown were identified using RepeatMasker by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Worley, K.C.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Worley, K.C., Yu, W., Chinault, C., Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gorrell,J.H., Haywood,M., Hernandez,J., Jackson,L., Jin,S., Kampal,R., Karpathy,S., Kovar,C., Leal,B., Lil,Y., Lichtarge,O., Liu,W., Logcn,O., Lu,J., Ly,T., Martinez,C., Oswal,G., Perez,L., Rashid,N.D., Rowland,K., Savage,L., Scherer,S.E., Shen,H., Simco,M., Stovall,K., Timms,K.M., Todd,J., Vo,Q., Williamson,A., Worley,K.C., Yu,W., Chinault,C., Nelson,D. and Gibbs,R.A.
                                                                                                                                                                                                                                                                                                                                                                                        Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                       Worley, K.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (bases 1 to 190482)
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Exon/Intron boundaries of identified genes were chosen if there were canonical splice junctions that maintained sequence continuity across the splice junctions.

Location/Qualifiers

Sequence similarities were identified using Powerblast by Jinghui

repeat\_region source complement(5523. .5825 complement(5266. complement (3017. complement(1171. .1209)
/rpt\_family="AT\_rich"
complement(2277. .2568) complement (693. complement(386. complement(4927. complement (211. /rpt\_family=' complement(4715 /rpt\_family="L2" rpt\_family="AluSg/x" /chromosome="X" /db\_xref="taxon:9606" /clone="GSHB-45N23" rpt\_family-"Alusg" rpt\_family="AluJb" rpt\_family="AluJb" map-" clone\_lib="Genome Systems Human BAC library" 'organism="Homo sapiens" \_family="Alusx"
lement(60) family-"TIGGER2" \_fami] \_family="AluSx" family-"MER46" \_family="TIGGER2" family-"Alusx" Xp22" y-"TIGGER2" "TIGGER2" .4571) .4754) .5221) 5390)

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                                                                                      /rpt_family="AluSq"
complement(16019. .16320^
/rpt_familv=""."
                                                                                                                                                                          /standard_name="DXS7171"
/note-"This STS has one fixed primer one non-specific primer that matches 14913, 14943, and 14973."
complement(14952..15154)
/rpt_family="L2"
                               complement(17350 .17651)
/rpt_family="Alusp"
                                                                                                                                               complement(15169..15425)
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/rpt_family="L2"
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1-143 of cDNA are not found in this clone"
complement(8918. .9217)
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/rpt_family="LIMC4"
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/rpt_family="AT_rich"
complement(10888...10908)
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complement(5940. .6
      rpt_family="AluJo/FRAM"
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lement(14220
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lement(14681. .14799)
_family="L2"
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lement(9960. .10)
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. .10430
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ement(7417
                                                                                                                                                                                                                                                                    family="(GGA)n"
. .15066
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11y="Alusq"
1. .8684,12419. .12527,12842. .12898,16964. .17002,
18049,24408. .24621,27318. .29047,31462. .31988)
19677"
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                                             SECTENT
SOURCE
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ECRHSFEX6
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DEFINITION
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KEYWORDS
REFERENCE
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U15127.1
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    Escherichia.
                      Escherichia coli
Escherichia coli
Escherichia proteobacteria; gamma subdivision; Enterobacteriaceae;
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6
   (bases 1 to 2402)
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%complement(18965, .19012)
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28387. .28
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complement(20165. .20456)
/rpt_family=""(TA)n"
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complement(26719. .26883)
/rpt_family="(CATA)n"
complement(27499. .27802)
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/rpt_family="L1M4"
complement(30725...31020)
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complement(24025.
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complement/occidents
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1, 27879
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8. .23360
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Pred. No. 3;
0; Mismatches 50
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and ORF f202 genes.
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TITLE
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TITLE
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 224
                    TATAGATGATATTGGAATATTTGCATTGGCAATGTGTAATGGAGAATCAATTAACGAGAA 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Direct Submission Submitted (26-SEP-1994) Charles
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Reshuffling of Rhs components to
J. Bacteriol. 177 (5), 1393-1398
95173120
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                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (bases 1 to 2402)
                                                                                                                                                                                705
                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                             complement(1879. .>2402)
/note="identified by similarity to E. coli K-12 sequence:
GenBank Accession Number L19201"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Penn State College of PA 17033, USA
                                                                                                                                                                                                              /translation="ISRSSQSKAIQLATHSDYSHTGMLVMRNKKPYVFEAVGPVKYTP
LKQWIAHGEKGKYVVRRVEGGLSVKQQQKLAQTAKRYLGKPYDFSFSWSDDRQYCSEV
VWKYYQNALGMRYGEQQKLKEFDLSSPQVQAKLKERYGKNIPLEETVVSPQAVFDAPQ
                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="end of RhsF genetic element and begining similarity between ECOR-50 and K-12 chromosomes"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /translation="npHQLQQLIRLPGQQYDEESGLYYNRHRYYDPLQGRYITQDPIG
LKGGWNFYQYPLNPISNIDPLGLYEFKSKNIDDIGIFALAMCNGESINENKEYGGLIC
KKQGEYFPMNPISSNDNDSVDLRNIKCPEGSERVGDYHTHGFYSDDKGNKVTKENDVY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Escherichia coli"
/insertion_seq="iso-IS1"
/strain="ECOR-50"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="ORF downstream of RhsF core with possible signal
peptide for export from cytoplasm"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DSLNFSSKDLTNSYMNGMGKKEYSSYLGTPNNTYLKYNPKAKGNGVTIIRQGSN"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /db_xref="taxon:562"
1877
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /translation="MKVIQCCYFLALVSSHLMAGVMSDDNIFLSNSDLAALYCVAKIF
PDGENILIYKVNIINASSKKDVFFYESPTSTHNDIMGGGGMSYAYEYDVKYNICHLRK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /function="extended core
/product="RhsF"
                                                                                                                                                                                                                                                                      /db_xref-"GI:564001"
                                                                                                                                                                                                                                                                                   /protein_id="AAA66217.
/db_xref="PID:g564001"
                                                                                                                                                                                                                                                                                                                            /product="ORF-f202"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'product-"unknown"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            transl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /strain="ECOR-50"
/db_xref="taxon:562"
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                                                                                                                                                                                                                                                                                                                                          transl_table=11
                                                                                                                                                                                                                                                                                                                                                            codon_start=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       protein_id="AAA66215.1"
db_xref="PID:g563999"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            codon_start=3
transl_table=11
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                                                               Score 42.4; DE Pred. No. 9.5; 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TAAAGAATATGGTGGGCTAATATGTAAGAAGCAAGGTGAATATTTCCCCCATGAATCCGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAGTTCAAATGATAATGATAGTGTAGACTTGCGAAATATAAAATGCCCTGAAGGTTCAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (26-JAN-1998) Biochemistry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rhs elements comprise three subfamilies which acquisition by Escherichia coli J. Bacteriol. 180 (16), 4102-4110 (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Wang
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria; Proteobacteria; gamma subdivision;
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Location/Qualifiers
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                                                                                                                            HYGYDEKGRLTGERQTVHHPQTEALLWQHETRHAYNAQGLANRCIPDSLPAVEWLTYG
SGYLAGMKLGDTPLVEYTRDRLHRETLRRFGRYELTTAYTPAGQLQSQHLNSLLSDRD
                                                                                                                                                                                                                EGLSQYRAYDSRGQLIAVKDTQGHETRYEYNAAGDLTTVIAPDGSRNGTQYDAWGKAI
                                                                                                                                                                                                                                                                                                                                                                                                       /translation="msgkpaarqgdmtqyggsivqgsagvrigaptgvacsvcpggvr
sghpvnptLgakvtpgEtDIALpgptpFILsRTySsyrTkTpapvgStgpgwkmpabI
ICDHRGLPLALISTEGATAWCAEYDEWGNLLNEENPHQLQQLIRLPGQQYDEESGLYY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="RhsF accessory genetic element"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'db_xref="taxon:562"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                organism-"Escherichia
                                                              |RLVHYTRTQYEEPLVESRYLYDPLGRRVAKRVWRRERDLTGWMSLSRKPQVTWYGWD
                                                                                                                                                                                                                                                                                                                                                                   LPEELRLSPHRYLATNSPQGPWWLLGWCERVPEADEVLPAPLPPYRVLTGLVDRFGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                     'db_xref="GI:2920637"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'product="core protein"
'protein_id="AAC32473.1"
'db_xref="PID:g2920637"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              transl_table=11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                strain-"ec45"
                                                                                    HPDSTLSMWPDNRIARDAHYLYRYDRHGRLTEKTDLIPEGVIRTDDERTHRYHYDSQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  codon_start=1
                                                                                                                                                                      TTQGGLTRSMEYDAAGRVIRLTSENGSHTTFRYDVLDRLIQETGFDGRTQRYHHDLT
KLIRSEDEGLVTHWHYDEADRLTHRTVNGETAEQWQYDERGWLTDISHISEGHRVTV
                                                                                                                                                                                                                                                                               FTYDDKYRGRMVAHRHTGRPEIRYRYDSDGRVTEQLNPAGLSYTYQYEKDHITITDS
DRREVLHTQGEAGLKRVVKKEHADGSVTQSQFDAVGRLKAQTDAAGRTTEYSPDVVT
                                                                                                                                                                                                                                    IDNPHSDLPCATDDATGSRKTMTWSRYGQLLSFTDCSGYVTRYDHDRFGQVTAVHRE
                                                                                                                                                                                                                                                                                                                         GYTEYGRDNGIRLSAVWLTHDPEYPENLPAAPLVRYGWTPRGELAVVYDRSGKQVR
                                                                                                                                                                                                                                                                                                                                                                                       .QLRDNTLILSDNGGRSLYFEHLFPGEDGYSRSESLWLVRGGVAKLDEGHRLAALWQ
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Hershey, PA 17033,
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Job time: 7290 sec
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Matches 94; Conservative
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                                                                                                      4057 AAGTTCAAATGATAATGATAGTGTAGACTTGCGAAATATAAAATGCCCCTGAAGGTTCAGA 4116
                                                                                                                                                                                          3997 TAAAGAATATGGTGGACTAATATGTAAGAAGCAAGGTGAATATTTACCCATGAATCCGAT 4056
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/note="similar to insertion element iso-IS1 of Shigella dysenteriae"
a 1731 c 1847 g 1380 t
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3917. .4357
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PDGENILIYKVNIINASSKKDVFFYESPTSTHNDIMGGGGMSYAYEYDVKYNICHLRK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 note="encodes core-extension ext-f3"
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                                                                                                                                                                                                                                                                                                                                                             Score 42.4; DB 2; Length 6577; Pred. No. 7.8; 0; Mismatches 86; Indels 0
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# GenCore version 4.5 Copyright (c) 1993 - 1998 Compugen Ltd.

OM nucleic nucleic search, using sw model

Run on: January 20, 2000, 05:08:09; Search time 123.5 Seconds (without alignments) 3117.778 Million cell updates/sec

Title: Perfect score: US-09-077-817-1 1539 ggtgcctgtcggcggggaga.....aatttttcttgcgaatgttg 1539

Scoring table:

IDENTITY\_NUC

Searched: 311585 seqs, 125096042 residues

Database : N\_Geneseq\_36:\*

Word size :

0

Number of hits that pass the threshold :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

	39	38	37	36	c 35	w	33	c 32	31	w	c 29	N	27	26	25	c 24	23	N	c 21	N	19	18	c 17	16	15	14	13	12	11	10	9	œ	7	6	<sub>5</sub>	4	ω	2	ч	No.	Result
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Query Match 100.0%; Score 1539; Rest Local Similarity 100.0%; Pred. No. 0; Macches 1539; Conservative 0; Mismatches

DB 1; Length 1539;

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1 ggtgcctgtcggcggggagaggggagatatcaaggttttaaatctcggagagaatggctta 60 GGTGCCTCTCGGCGGGGAGAGAGGCAATATCAAGGTTTTAAATCTCGGAGAAATGGCTTA 60

181 tgagata/ggattatgaagagaacccggatacttaggttatctctatttgcaatggcaa 240

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# ALIGNMENTS

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requence 11319 SP; 492 A; 247 C; 335 G; 465 T;	ich is not the same as that shown	used to identify ligands and modulators of IL-13R. Note: IL-13R beta	ering to receptors; when coupled to a toxin also for treatment of everproduction of IL-13R. Cells that express IL-13R at the surface are	immenoassays) to diagnose diseases associated with abnormal expression	allergy. II-13 receptors are also useful as antisense molecules for gene therapy (blocking synthesis of IL-13R). Antibodies are used (in standard	regulate IL-13-induced responses for treatment of inflammation and	and alpha which can be used as IL-13 antagonists, specifically to		diagnostic probes to identify aberrant synthesis or genetic anomalies	recenter Nucleic acids encoding II-13E beta and alpha are used as	The IL-13R beta has high affinity for IL-13 while IL-13R alpha has low affinity, but acquires high affinity when associated with the IL-4	and 427 as proteins are designated IL-13R beta and alpha respectively.	ació sequences, which are receptors for interleukin-13 (IL-13); the 380	invention relates to new purified peptides comprising 380 or 427 amino	This sequence encodes human interleukin-13 (IL-13) beta receptor. The	2	f inflammation	New purified human interleukin-13 receptors - and related nucleic	P-PSDB; 1/249/2.	97-319773/29.	Taurent	(SNET ) SYNOET SY	07-NOV-1596; F01756.	12-JUN-1997	W09720926-A5		Interleukin-13 receptor; diagnosis; inflammation; allergy, IL-13; ss.	uman inter	22-JUN-1998 (first entry)		T85826 standard: DNA: 1539 BP.	RESULT 1

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Length 1298; Indels

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PS Claim 6; Figure 2a: 83pp; French CC This sequence encodes human interleukin-13 (IL-13) beta receptor. The CC invention relates to new purified peptides comprising 380 or 427 amino and 427 am proteins are designated IL-13R beta and alpha respectively. CC affinity, but acquires high affinity when associated with the IL-4 CC alids encoding IL-13R beta and alpha are used as receptor. Nucleic acids encoding IL-13R beta and alpha are used as CC such as loss of heterozygosity aberrant synthesis or genetic anomalies. They are also used for production of recombinant IL-13R beta and alpha are used as IL-3 induced responses for treatment of inflammation and communoassays) to diagnose diseases associated with abnormal expression. CC of IL-13 receptors are also useful as antisense molecules for gene communoassays) to diagnose diseases associated with abnormal expression. CC used to identify ligands and modulators of IL-13R. Note: IL-13R beta correspondention of IL-13R. Cells that express IL-13R. Note: IL-13R beta correspondention (T86464), which is not the same as that shown in the sequence listing (T85826).

Sc Sequence 1298 BP; 407 A; 231 C; 266 G; 394 T;
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Human interleukin-13 beta
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ds, useful for diagnosis and treatment of inflammation, allergy,
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New nucleic acid encoding interleukin-13 receptor binding chain and transformed cells - proteins, antibodies and inhibitors, for treating immunoglobulin E-mediated diseases, e.g. Graves disease, and in diagnosis and in diagnosis are chain of the interleukin-13 receptor, designated IL-13bc IL-13bc acts a mediator of the known biological activities of IL-13. The present sequence encodes the human interleukin-13 receptor are used to mediator of the known biological activities of IL-13. The present sequence was isolated from human testis library. Recombinant IL-12bc proteins, and antibodies raised against them, are used to inhibit the binding of IL-13 to its receptor. They are particularly used to reet IgE-mediated conditions, e.g. allergy, asthma and immune complex discreters, especially lupus, nephritis, thyroiditis and Grave's disease. They are also used to treat immune deficiency (particularly in insematopoietic progenitor cells), cancer etc., and to increase macrophage activation, e.g. in yaccination. To potentiate IL-13 activity, a protein of the such activity is combined with IL-13bc and the mixture applied, in vivo, to a cell expressing at least one chain of the IL-13 receptor.
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04-SEP-1997.
028-FEB-1997. U03124.
R 01-MAR-1996: US-609572.
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COMMY) GENETICS INST INC.
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WPI: 97-418632/41.
P-PSDB; W35295.
New nucleic acid en
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Best Local Similarity 84.3%;
Matches 1292; Conservative
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         gttaaacctttgccgccagtcagttggaaatatcttacttttactcgggagaggttcatgt 961
                              ggagcagtgaggcatcagactataaagatttctatatttgtgttaatggatcatcagaga
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1369 BP; 436 A; 247 C; 282 G; 404 T;
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Pred. No. 2e-222;
0; Mismatches 0,
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ental polyat kwa. The resulting polypeptide is a receptor ic	claic acid encoding testis-specific cytokine receptor claic acid encoding testis-specific cytokine receptor entification of ligands or antagonists, potentially fontraceptives or for infertility treatment properties or for infertility treatment 1; Page 44-46; 79pp; English.  DNA sequence encodes a novel ligand-binding receptor, shares homology with cytokine receptors and is isolate that the properties of t	Jartner Jartner 1 PJ; 197-4708	/*tag- /produc /produc 33913-Al /note= 8EP-1997, NR-1997, UU4043. AR-1996; US-013345.	(first e 2 cytokin eptor; li antagoni Locat	LT 82 196	502 atgagictcaataaactgaattttcttgcgaa 1 	1382 aacacctacccaaaatgattccagaatttttctgtgatacatgaagaagatttgcatct 1441	100 GTGAAGACCTATCGAAGAAAACTTTGCTA	202 gatgacggaatttgggcas 	1082 tgactgctacagttgaaaatgaaacatacaccttgaaaacaacaaatgaaacccgaataa 1141	GAAATTAAGCTGAAATGGAGCATACCTTTG	aaattaagotgaáatggagcatacotttgtttaggogtggacotattocagcaag

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Best Local Similarity 83.1
Matches 1284; Conservative
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Sequence 1289 BP; 407 A; 236 C; 258 G; 388 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              of testicular cells, probably being involved in spermatogenesis. It can be used to detect ligands that promote proliferation and/or differentiation of such cells in cultures and may also be used to tree infertility. Antagonists of this receptor may be used to characterise ligand-receptor interactions, and as male-specific contraceptives. By blocking the action of IL-13, receptor antagonists and ligand-binding this receptor can also be used to modulate immune function, e.g. in
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Pred. No. 1.9e-21
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EP-812913-A2.
17-DEC-1997.
04-JUN-1997; 3
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                                                                                                                                                                                                                                                                                                                                     O8-JUN-1998 (first entry)
Human cytokin-/peptide receptor, HR-1 receptor cDNA.
HR-1 receptor; cytokine receptor; peptide hormone re
infection; bi.n; trauma; asthma; allergy; AIDS; apla
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                                                                                            mat_peptide
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08-JUN-1998
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claimed (Claim
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CC This cDNA clone codes for a novel human cytokine/peptide hormone coeptor, designated HR-1 receptor (see W41502). Plasmid ATG-531, creceptor (see W41502). Plasmid ATG-531, comparising HR-1 receptor contained in vector pBluescript SK+, colisated from a human testis cDNA contained in vector pBluescript SK+, colisated from a human testis cDNA library. Also claimed are a colisated from a human testis cDNA contained comprising the comprising amino acids 1-380 or 22-380 of the 380 cresidue HR-1 receptor amino acids sequence, a vector comprising compressing the polypeptide, and an antagonist to the compression compressing compression contains and compression compression contains contai
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Best Local Similarity
Matches 1271; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12-JUN-1996; US-017843.
(HUMA-) HUWAN GENOME SCI INC.
(SMIK ) SWITHKLINE BEECHAM CORP.
Appelbaum ER, Hu J;
PDC-28-034974/04.
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84.1%;
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Pred. No. 1e-216;
0; Mismatches 0; Indels 24
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Ş 8 Š В Ş 밁 Ş ₽

V02295 standard; cDNA; 1288 BP. V02295; .08-JUN-1998 (first entry) .Homo sapiens cDNA encoding the HR-1 receptor.

533 gyttaaattatytciggitatticcttgataccaattaccaacttgititactggtatgagg 682 514 GGT

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PT DNA encoding human cytokine-peptide hormone receptor - useful for preventing preventing or diagnosing, e.g. lowered resistance to infection, asthma, allergy, or haematopoietic disease Claim 1; Fig 1; 75pp; English.

CC (HR-1 receptor). This, or it's activators or agonists, can be used to treat, prevent or diagnose predisposition to lowered resistance to complete the prevent or diagnose predisposition to lowered resistance to induced by acquired immune deficiency syndrome (AIDS), aplastic anaemia, concurropaenia or cytotoxic treatments for cancer. Antagonists of the conditions associated with overexpression of the HR-1 receptor, e.g. antibodies or fragments of it may be used to treat conditions associated with overexpression of the HR-1 receptor, e.g. those listed above. Antibodies may also be used to assay levels of HR-1 creceptor, overexpression of which may be diagnostic of tumours, by usual immunoassays; to isolate and identify HR-1 receptor. The nucleotide sequence conditions for isolating genomic HR-1 clones, PCR primers, diagnostic condentification and mapping.

So sequence 1288 BP; 421 A; 227 C; 252 G; 388 T;
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Best Local Similarity
Matches 1271; Conser
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18-DEC-1997.
09-UTL-1996; U11459.
12-UUN-1996; WO-U10262.
12-UUN-1996; U5-017843.
(HUMA-) HUMAN GENOME SCI INC (SMIK ) SMITHKLINE BEECHAM C Appelbaum ER, Hu J;
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CDS
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Pred. No. 1e-216;
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PT Nucleic acid sequence encoding human cytokine peptide hormone Preceptor - useful to treat, prevent or diagnose, e.g. lowered PT receptor - useful to treat, prevent or diagnose, e.g. lowered PT resistance to infection, asthma, allergy or haematopoietic disease CC claim 4; Page 61-62; 76pp; English.

CC cytokine/peptide hormone receptor, designated the HR-1 receptor CC cytokine/peptide hormone problem to the recombinant CC cytokine/peptide hormone problem to the recombinant CC cytokine/peptide hormone problem to the recombinant CC cytokine/peptide hormone problem to the receptor problem to isolate CC genomic HR-1 receptor, as a source of problem to isolate CC diagnostic reagent (particularly to detect gene mutations which CC identification and mapping, and in a claimed method for treating CC apatient having need of HR-1 receptor. HR-1 receptor activators CC and agonists can be used to treat, prevent or diagnose CC and agonists can be used to treat, prevent or diagnose CC or haematopoletic disorders, e.g. where induced by AIDS, aplastic CC anaemia, neutropaenia or cytotoxic treatments for cancer.

SQ Sequence 1288 Bp; 421 A; 227 C; 252 G; 388 T;
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Best Local
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(HUMA-) HUMAN GENOME SCI INC.
(SMIK) SMITHKLINE BEECHAM CORP
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RESULT
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                                                                                                                                                                                                 CC This sequence encodes a novel ligand-binding receptor, Zcytor2, which CC shares homology with cytokine receptors and was isolated from a human CC testis cDNA library. The resulting polypeptide is a receptor for CC cytokines (particularly interleukin-13) and is expressed on the surface CC of testicular cells, probably being involved in spermatogenesis. It can CC be used to detect ligands that promote proliferation and/or CC differentiation of such cells in cultures and may also be used to treat CC infertility. Antagonists of this receptor may be used to characterise CC ligand-receptor interactions and as male-specific contraceptives. By CC blocking the action of II-13, receptor antagonists and ligand-binding CC this receptor can also be used to modulate immune function, e.g. in CC allergy and asthma, as a diagnostic to determine circulating levels of CC ligand and also to isolate and purify ligands. Antibodies can be used to assay circulating receptor (an abnormal level may be indicative of CC disease such as cancer), for labelling cells that express the receptor, CC and therapeutically as antagonist.

Sequence 1167 BP; 365 A; 213 C; 233 G; 356 T;
                                                                                                                         Query Match
Best Local Similarity
Matches 1137; Conser
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18-SEP-1997.
12-MAR-1997: U04043.
13-MAR-1996: US-013345.
(ZYMO) ZYMOGENETICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New nucleic acid encoding testis-specific cytokine receptor for identification of ligands or antagonists, potentially for male contraceptives or for infertility treatment Claim 2; Page 49-51; 79pp; English.

This sequence encodes a novel ligand-binding receptor, Zcytothis sequence encodes a novel ligand-binding receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human Zcytor2 cytokine receptor cDNA.
Cytokine receptor; ligand binding; testi
infertility; antagonist; contraceptive;
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CC which shares homology with cytokine receptors and is isolated from CC which shares homology with cytokine receptors and is isolated from CC is a receptor for cytokines (particularly interleukin-13) and is conversed on the surface of testicular cells, probably being involved in CC expressed on the surface of testicular cells, probably being involved in CC expressis. It can be used to detect ligands promoting proliferation CC and/or differentiation of such cells in cultures and may also be used to treat infertility. Antagonists of this receptor may be used to contraceptives. By blocking the action of IL-13, receptor antagonists and CC injund-binding this receptor interactions and as male-specific contraceptives. By blocking the action of IL-13, receptor antagonists and CC injund-binding this receptor and also be used to modulate immune cc circulating levels of ligand and also to isolate and purify ligands. CC may be indicative of disease such as cancer), for labelling cells that cappess the receptor, and therapeutically as antagonist.

Sequence 1126 BP; 359 A; 191 C; 227 G; 349 T;
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12-SEP-1997: U04043.
13-MAR-1996; US-013345.
(ZYMO ) ZYMOGENETICS INC.
Baumgartner JW, Farrah TM, Foster DC, Grant FJ.
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Cytokine receptor; ligand binding; testicular cell; spermatogenesis;
infertility; antagonist; contraceptive; diagnostic; therapeutic; ds.
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P-PSDB; W36616.
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                                                                                                                                                                     Score 624; DB 1;
Pred. No. 1.2e-160;
0; Mismatches 50;
                                                                                                                                                                                                     Length 1126;
                                                                                                                                                                     Indels
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107	•				•					**	•			•					
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	taaacaatgotgggaaggtgaagacctatcgaagaaaactttgctagtagctgggatcg 13	tgantatttattgctcagatgacggaatttgggcaaaggaatcaagtagtgagtg	aaatgaaacccgaataatagagtttttagtagcaattatgctttgtagtaagaagcaaa 1               AAATGAAACCCGA	gcatggaggaattttggtgactgctacagttgaaaatgaaacátácaccttgaaaacaa 1 	Ctattccagcaagġtgttttgattatgaaattgagatcagagaagatgatactaccgaa 10 	Ctcgggagagttcatgtgaaattaagctgaaatggagcatacctttgtttaggcgtgga 1 	ttcagcttcaaaatatagttaaacctttgccgccagtcagt	taatggatcatcagagaacaagcotgaaatatcaaggaatcagatccagttatttcact 88	ccctatttggcaataaaggagcagtgaggcatcagactataaagatttctatatttgtg 82    -        CCTATTTGGAGTCATCAGACTATAAAGATTTCTACATTTGTG 65	atttggaaacagtgtgttgattacatcaaggctgatggacaaaatataggatgcagatt 76 	Cttgataccaattacaacttgttttactggtatgagggcttggatcatgcattaaata 70 	attggcaatatttactctgttcttggaaacctggcataggttacattatgtctgggtac 6 	gaattccagaaactaaagttcaggattaagttttgggtagaatggattgcgtatattac 58 	aagttcaaagttccaattgctaggagtgggcagaaactacttattggatatcaccacaa 52                 AAGTTCAAAGTTCCTGGGCAGAAGCTACTTATTGGATATCGCCACAA 40	gaattatagaagggcgaagatacacacgcttttaccatggcaatgcacaaatggatca 46  -	ggttaccatcattactaagaatctacattacaaagatgggtttgatcttaacaagggca 40 	agtggaatatgaactaaaataccgaaacattggtagtgaaacatggaaggctagtgtag 34 	CTATTTGCAATGGCAACCCCCACTGTCTCTGGATAATTTTAAGGAATGCA 20	CCCACCTCAGGATTTTGAGATAGTGGATCCCGGATATTTAGGTTATC 15

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Best Loc
Matches
                                                                                                                                                                                                                                           New isolated interleukin-13 binding protein - used to develop products for therapy e.g. for allergic conditions such as asthma or for diagnosis or detection

Example 14; Page 50-52; 69pp; English.

The II-13 binding protein and related therapeutic molecules can be used in the antagonism of at least one II-13 activity. They can be used for treating II-13 mediated conditions such as certain allergic conditions such as asthma or to inactivate locally administered II-13 after II-13 treatment. The products can also be used as diagnostic agents, e.g. fo detecting autoimmune diseases. The antibodies can also be used for immunotherapy and may also be used as a diagnostic tool.

Sequence 1079 BP; 341 A; 209 C; 227 G; 302 T;
                                                                                                                                                                                                                                                                                                                                                                                          WO9810638-A1.
19-MAR-1998.
10-SEP-1997; A
27-FEB-1997; A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Construct containing mature interleukin-13 binding protein Therapeutic; IL-3 mediated condition; allergy; asthma; diaquitolimnune disease; antibody; immunotherapy; ss.
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Key
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16-SEP-1998
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/note= "No stop cc
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82.78;
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                                                                                                                                                                                                   Score 595; DB 1; Pred. No. 9.2e-153; 0; Mismatches 0;
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                   GCGAAGATACACACGCTTTTACCATGGCAATGC
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19-MAR-1998.
18-SEP-1997;
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16-SEP-1998 (first entry)
Mature interleukin-13 binding protein gene.
Therapeutic: IL-3 mediated condition: allergation autoimmune disease; antibody: immunotherapy;
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PA (AMRA-) AMRAD OPERATIONS PTY LTD.

PA (AMRA) AMR
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Best Local Similarity
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Query Match 18.
Best Local Similarity 85.
Matches 429; Conservative

18.6%; Score 287; DB 1; 85.6%; Pred. No. 4.8e-69; etive 0; Mismatches (

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o be useful for (); 92 G; 12	ctivity, receptor/ligand activity, anti-inflammatory acti adherin/tumour invasion suppressor activity, tumour inhib	hemotactic/chemokinetic activity,	suppressing activity, haematopoiesis regula	given. Suggested activities include nutritional activity, immune	for treating, preventing or ameliorating medical	<pre>tide, which is a secreted EST, and the encoded prot to have useful biological activities which would ma</pre>	present sequence represents a human expressed sequence tag	im 1; Page 320; 618pp; English.	/, pituitary, retina and	encoding human secreted proteins - derive	.,	Agostino MJ, Jacobs K, Lavallie ER, McCoy JM, Merberg D, Racie LA, Spaulding V, Treacy M:	CS INST INC.	10-APR-1997; US-838821.	MO9845436-A2.	SS	ind; thrombolytic; anti-inflammatory; cadherin; anti-tu	<pre>growth; activin; inhibin; chemotaxis; chemokinesis; haematopoiesis;</pre>	3)	,	789756 standard; cDNA; 456 BP.	T 12	TGAGTGGAGTGATAAACAATGCTGGGAAGGTGAAGACCTATCGAAGAAAACTTTGC	aaggtgaagacctatcgaagaaaact	A 883	gac	PATGAAACCCGACAATTATGCTTTGTA	taatagagtttttagtagcaattatgctt	ATACI	1052 gatactaccgaaagcatggaggaattttggtgactgctacagttgaaaatgaaacataca 1111	703GACCTATTCCAGCAGGTGTTTTGATTATGAAATTGAGATCAGAGAAGAT 753	992 tttaggcgtggacctattccagcaaggtgttttgattatgaaattgagatcagagaagat 1051	TTTG 7	tatottaottttaotogggagagttoatgtgaaattaagotgaaatggagoataoottt	592 AGTTATTTCACTTTTCAGCTTCAAAATATATAGTTAAACCTTTGCCGCCAGTC 643

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W09810638-A1.

19-MAR-1998.
10-SEP-1997; AU-005374.
27-FEB-1997; AU-005374.
110-SEP-1996; AU-005262.
(AMRA-) AMRAD OPERATIONS PTY LTD.
Hilton DJ, Nicola NA, Simpson RJ, Zhan
WPI; 98-207062/18.
P-PSDB, W56255, W56256, W56257.
New isolated interleukin-13 binding pr
products for therapy e.g. for allergic
for diagnosis or detection
The IL-13 binding protein and related
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Interleukin-13 binding protein C-terminal region
Therapeutic; IL-3 mediated condition; allergy; as
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T95213;
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                                                            (GEMY )
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28-FEE-1997; U03124
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The present sequence encodes the murine interleukin-13 (IL-13) binding chain of the interleukin-13 receptor, designated IL-13bc. IL-13bc acts a mediator of the known biological activities of FIL-13. The present sequence was isolated from the thymuses of 6.8 week old mice. Recombinant IL-13bc proteins, and antibodies raised against them, are used to inhibit the binding of IL-13 to its receptor. They are particularly used to treat IgE-mediated conditions, e.g. allergy, asthma and immune complex disorders, especially lupus, nephritis, thyroiditis and Grave's disease. They are also used to treat immune deficiency (particularly in CC chaematopoietic progenitor cells), cancer etc., and to increase macrophage activation, e.g. in vaccination. To potentiate IL-13 activity, a protein with such activity is combined with IL-13bc and the mixture applied, in vivo, to a cell expressing at least one chain of the IL-13 receptor continuous to detect expression of IL-13, its receptor or binding chain, and to raise specific antibodies which may be useful for treating some tumours.
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Best Local Similarity
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63.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 237.4;
Pred. No. 2.5e
0; Mismatches
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2.5e-55;
hes 201;
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19-MAR-1998.
10-SEP-1997; A
27-FEB-1997; A
                The II-13 binding protein and related therapeutic molecules can be used in the antagonism of at least one II-13 activity. They can be used for treating II-13 mediated conditions such as certain allergic conditions such as asthma or to inactivate locally administered II-13 after II-13 treatment. The products can also be used as diagnostic agents, e.g. for detecting autoimmune diseases. The antibodies can also be used for
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                                                                                              New isolated interleukin-13 binding protein - used to develop products for therapy e.g. for allergic conditions such as astifor diagnosis or detection Claim 10; Page 43; 69pp; English.
                                                                                                                                                                  10-SEP-1996; AU-002262.
(AMRA-), AMRAD OPERATIONS PTY LTD.
Hilton DJ. Nicola NA, Simpson RJ,
WPI; 98-207062/18.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Therapeutic; IL-3 mediated communotherapy; autoimmune disease; antibody; immunotherapy;
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24-SEP-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13 binding protein N-terminal region gene.
IL-3 mediated condition; allergy; asthma;
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/product= "IL-13 binding protein ORF
/note= "No start codon, stop codons ;
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446	422	388	362	341	302	290	242	241	182	193	122	133	62	76	2	Matches 352; Conserv	Query Match	Sequence	2
AGGTTA	aagata	AGAATC	agaatc	AATACC	aatacc	CCCCAC	ccccact	GAGATA	gagata		acaagc	TTCGTT	ttcgtt	GIGCCIC	gtgcct	352;	atch		
AGGTTACACACGGTTTT	aagatacacacgctttt	FACATT	tacattac	SAAACATT	yaaacatt	GTCTCTG	gtctctg	TGGAT	gtggatta	AC	tttgcac	rectreec	Lgcttggc	STCGGCGG	tcggcgg	Matches 352; Conservative	1 2 1 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	4/3 07,	77 55.
TTT 462	ttt 438	TACAAAGGAT	aaagatgggt	GGTAGTGAAA	ggtagtgaaa	GATCATTTT-	gatcattttg		tgaagagaac	TTCATCTTCA	ttcatcttca	TATCGGATGC	:tatcggatgo	GGAGAGAGGG	ggagagaggg	,	14.48;	104 27	104
		GGGGTTTG	ttgatctt	CATGGGAA	  catggaagg	<i>I</i>	tgttgtgaa	CCGGATACI	ccggatact:	GACACCGAC	lgacaccgag	TTATATAC	ttatataco	AATATCAAC	aatatcaag	0; Mismatches	Score 221	, ,	S .
		AGAATCTACATTTACAAAGGATGGGGTTTGGATCNTTAACAAGGGGCATTGAAGGCGA 445	agaatctacattacaaagatgggtttgatcttaacaagggcattgaattatagaagggcg 421	AATACCGAAACATTGGTAGTGAAACATGGGAAGGACCATCATTACTA	aataccgaaacattggtagtgaaacatggaaggctagtgtagaggttaccatcattacta	CCCCACTGTCTCTGGATCATTTTAAGGAATGCACAGTGGAATATGAACTAA	aggaatgcaca	TAGGTTATCTC	gagatagtggattatgaagagaacccygatacttaggttatctctatttgcaatggcaac	ACTTCATCTTCAGACACCGAGATAAAAGTTAACCCTCCTCAGGATTTTT	yataaaagttaa 	CTTTCTGATAAG	ttcgtttgcttggctatcggatgcttatatacctttctgataagcacaacatttggctgt	GETTTAAATCT	gtgcctgtcggcggggagagggcaatatcaaggttttaaatctcggagaaatggcttaa 61	ches 35;	Score 221.6; DB 1;	114 0,	11.6
		GGGCATTG	gaattatag	GACCATC	gttaccatc	GTGGAATAT	gtggaatat	TATTTGCAA	tatttgcaa	CCCTCCTCA	ccctcctca	CACAACATT	cacaacatt	CGGAGAAAT	cggagaaat	Indels	Length 473;	101 1,	131 7.
		AAGGCGA	aagggcg	ATTACTA	attacta	GAACTAA	gaactaa	TGGCAAC	tggcaac	GGATTTT	ggatttt	TGGCTGT	tggctgt 	GGCT	ggcttaa 	50; G	73;		
		445	421	387	361	340	301	289	241	240	181	192	121	133	61	Gaps			
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Search completed: January 20, 2000, 06:16:48 Job time: 4119 sec



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Title:
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1539
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Copyright (c) 1993 - 1998 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

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2.8	2.8	2.8	2.9	2.9	2.9	2:9	2.9	2.9	3.0	3.2	3.5	3.7	4.9	13.5	.14.4	15.5	. 15.8	16.3	. 19.5	19.7	27.7	Match	Query
859	1101	1101	1085	1101	1101	1101	1101	1101	1201	160	1204	1101	469	365	473	446	465	. 360	443	479	676	Match Length DB	
69	69	70	70	70	69	69	69	70	70	48	70	69	89	31	22	63	22	36	40	<b>4</b> 5	60	BB	
CNS004YY	CNS0100X	CNS017KX	CNS016YR	CNS017ZS	CNS0106X	CNS0039G	CNS00240	CNS0182P	CNS016FP	AI547789	CNS016E2	CNS0039G	AQ761600	AA298563	R52795	AW001800	R52796	AA621766	AA909507	AI358911	AI798934	ID	
		AL108171 Drosophil	AL107373 Drosophil	AL108706 Drosophil	AL098595 Drosophil	AL063921 Drosophil	ω	AL108811 Drosophil	AL106687 Drosophil	AI547789 UI-R-C3-s		AL063921 Drosophil	AQ761600 HS_3132_B	AA298563 EST114178	R52795 yg99f10.r1	AW001800 ws05c01.x	R52796 yg99f10.s1	AA621766 af06d10.s	AA909507 ol16d11.s	AI358911 qy19c05.x	AI798934 we94e04.x	Description	

126;

Gaps

10;

860

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Email: Robert_Strausberg@nih.gov
This clone is available royalty-free through LLNL;
                                                                                                                                                                                                                                                                                                                                             Contact: Robert Strausberg, Tel: (301) 496-1550
                                                                                                                                                                                                                                                                                                                                                                                                    Tumor Gene Index
Unpublished (1997
                                                                                                                                                                                                                                                                                                                                                                                                                     NCI CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eutheria; Primates; 1 (bases 1 to 676)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AI798934 676 bp mRNA EST 06-JUL-1999 we94e04.x1 Soares_NFL_T_GBC_S1 Homo sapiens CDNA Clone IMAGE:2348766 3' Similar to SW:I132_HUMAN Q14627 INTERLEUKIN-13 AI798934
                                                                                                                                                                                                                                                                                                MAGE Consortium
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                                                                                                                                                                                                                                                                              E Consortium (info@image.llnl.gov) for primer: -40UP from Gibco
                                                                                                                                                                                                                                                                 quality sequence stop:
       /note="Torgan: pooled; Vector: pTTT3D-Pac (Pharmacia) wit a modified polylinker; Site_1: Not I; Site_2: Eco RI; Equal amounts of plasmid DNA from three normalized libraries (fetal lung whit19W, testis NHT, and B-cell NCI_CGAP_GCB1) were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driv was PCR-amplified cDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of I.M.A.G.E. clones 297480-302087, 682632-687239,
                                                                                                                                                                        /Organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2348766"
/clone_lib="Soares_NFL_T_GBC_S1"
                                                                                                                                                                  /lab_
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Best Local Similarity 82.6%;
Matches 660; Conservative *
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                                                                                                                                                                                                                              TTCCAGAATTTTTCTGTGATACATGAAGA------
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479 bp mRNA EST 15-FEB-1999 qy19c05.x1.NCI_CGAP_Brn23 Homo sapiens cDNA clone IMAGE:2012456 similar to SW:1132_HUMAN Q14627 INTERLEUKIN-13 RECEPTOR ALPHA-2 CHAIN PRECURSOR; mRNA sequence.
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Soares and M. Fatima Bonaldo. "
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Pred. No. 3.5e-92;
0; Mismatches 13
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JOURNAL COMMENT

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REFERENCE AUTHORS

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SOURCE ORGANISM

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                1025 gattatgaaattgagatcagagaagatgatactaccgaaagcatggaggaatttttggtga 1084
                                                                                                                                                                                                             479 ATTAAGCTGAAATGGAGCATACTTT---
                                                                                                                                                                                                                                965 attaagctgaaatggagcatacctttgtttaggcgtggacctattccagcaaggtgtttt 1024
                                                                                                                                                                                                                                                                                                    Local Similarity
                                                                                           ctgctacagttgaaaatgaaacatacaccttgaaaacaacaaatgaaacccgaataatag 1144
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AI358911.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Seq primer: -400P from Gibco
High quality sequence stop: 324.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 479)

NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National cancer Institute / National Institute of Neurological Discorders and Stroke, Brain Tumor Genome Anatomy Project (CGAP/BTGAP), Tumor Gene Index
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: Robert_Strausberg@nih.gov
Tissue Procurement: David N. Lou
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished (1998)
On Aug 21, 1998 this sequence version replaced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Insert Length: 1039
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     www-bio.llnl.gov/bbrp/image/image.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA Sequencing by: Washington University Genome Clone distribution: NCI-CGAP clone distribution found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bonaldo,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cDNA Library Arrayed by: Greg Lennon,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                primer
                                                                                                                                                                                                                                                                                                                                                                                            144
                                                                                                                                                                                                                                                                                     Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           adaptors (Pharmacia), digested with Not I
the Not I and Eco RI sites of the modified
Library is normalized, and was constructed
Soares and M.Fatima Bonaldo."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone="IMAGE:2012456"
/clone_lib="NCI_CGAP_Brn23"
/tissue_type="glioblastoma (pooled)"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /db_xref="taxon:9606"
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 CAATTATGCTTGTAGTAAGAAGCAAAGTGAATATTTATTGCTCAGAT
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1.2e-62;
hes 11;
                                                                                                                                                                                                             TGGGCCCTATCCAGCAAGGTGTTTT 430
                                                                                                                                                                                                                                                                                                                                                                                                                           the modified pT7T3 vector. constructed by Bento
                                                                                                                                                                                                                                                                                                                   Length 479;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This clone is available royalty-free through LINL; contact the IMAGE Consortium (info@image.logo) for further information. Insert Length: 609 Std Error: 0.00 Seq primer: -40ml3 fwd. Er from Amersham High quality sequence stop: 220.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
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1 (bases 1 to 443)
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/note=Torgan: pooled; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; Equal amounts of plasmid DNA from three normalized libraries (fetal lung NbHL19W, testis NHT, and B-cell NCI_GGAP_GCB1) were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of I.M.A.G.E. ciones 297480-302087, 682632-687239, 726408-728711, and 729096-731399. Subtraction by Bento
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/clone="TMAGE:1523637"
/clone_lib="Soares_NFL_T_GBC_S1"
/lab_host="DH10B"
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                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 360)

Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,; Krizman,D., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Krizman,D., Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B., White,Y., Wylle,T., Waterston,R. and Wilson,R. WashU-NCI human EST Project

WashU-NCI human EST Project

Unpublished (1997)
            Washington University Scho
4444 Forest Park Parkway,
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                   AA621766 360 bp mRNA af06d10.s1 Soares_testis_NHT Homo
                                                             Contact: Wilson RK
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est@watson.wustl.edu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       agaaaactttgctagtagctgggatcgtttctggctaccatttggtttcatcttaatatt 1336
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     465 bp
yg99f10.s1 Soares infa
IMAGE:41648.3', mRNA so
R52796
                                                                                                                                                                                                                                                                                                                                                                                      ATGATTCCAGAATTTTTCTGTGATACATGAAGA----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AGTTATATTTGTAACCGGTCTGCTT-----TTGCGTAAGCCAAACACCTACCCAAAA 131
                                                     g814698
R52796.1 GI:814698
Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              primer: -40m13 fwd. ET from Amersham h quality sequence stop: 242.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library went through one round of normalization to Cot5, and was constructed by Bento Soares and M. Fatima Bonaldo. "68 c 61 g 121 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand was prepared from mRNA obtained from Clontech
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Laboratories, Inc., and primed with a Not
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/db_xref="taxon:9606"
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55 Std Error: 0.00
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Best Local
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                                                                                                                                                                                                                                                                                           1088 ctacagttgaaaatgaaacataca-ccttgaaaacaacaactgaaacccgaataatagag 1146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  source
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                                                                                                              agacctatcgaagaaaactttgctagtagctgggatcgtttctggctaccatttggtttc 1325
                                                                                                                                                                                                    acggaatttgggcaaagaatcaagtagtgagtggagtgataaacaatgctgggaaggtga 1265
                                     atcttaatattagttatatttgtaaccggtctgcttagtgaatgttgcgtaagccaaaca
                                                                                                                                                                                                                                                                                                                                                             CTACAGTTGAAAATGAAACATACACCCTTGAAAAACAACAAATGAAACCCGACAATTATGC 346
                                                                                                                                                                             ACGGAATTTGG------AGTGAGTGGAGTGATAAACAATGCTGGGAAGGTGA
                                                                                         AGACCTATCGAAGAAAACTTTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                        381;
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4444 Forest Park Parkway, Box 8501, St. Louis, MO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chissoe, S., Dietrich, N., DuBuque, T., Favello, A., Gish, W., Hawkins, M., Hultman, M., Kucaba, T., Lacy, M., Le, M., Le, N., Moore, B., Morris, M., Parsons, J., Prange, C., Rifkin, L., Rohlfing, T., Schellenberg, K., Soares, M.B., Tan, F., Thierry-Meg, J., Trevaskis, E., Underwood, K., Wohldmann, P., Waterston, R., Wilson, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Seq primer: Promega -21m13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  High quality sequence stops: 382 Source: IMAGE Consortium, LINI This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information insert Length: 1454 Std Error: 0.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: est@watson.wustl.edu
Insert Size: 1454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Generation and analysis of 280,000 human expressed sequence tags
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hillier,L., Lennon,G., Becker,M., Bonaldo,M.F., Chiapelli,B., Chissoe,S., Dietrich,N., DuBuque,T., Favello,A., Gish,W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Wilson RK
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  double-stranded cDNA was ligated to Hind III adaptors (Pharmacia), digested with Not I and directionally cloned into the Not I and Hind III stles of the Lafmid BA vector. Library went through one round of normalization. Library constructed by Bento Soares and M.Fatima Bonaldo."

2 79 g 158 t 1 others
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vacTGGAAGAATTTTTTTTTTTTTTTTTT 3'];
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/note="Organ: whole brain; Vector: Lafmid BA; Site_1: Not
1; Site_2: Hind III; 1st strand cDNA was primed with a No
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   organism="Homo sapiens"
/db_xref="GDB:414189"
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                                                                                                                                                                                                                                                                                                                                                                                                                  Seg primer: -40UP from Gibco High quality sequence stop:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    On May 18, 1998
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Emmert-Buck, M.D., Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact:
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National Cancer Institute, Cancer Genome Anatomy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CONA Library Preparation: M. Bento Soares, Ph.D. cDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cione distribution: NCI-CGAF clone distribution through the I.M.A.G.F. Consortium/LLNL at:
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                      136
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Robert_Strausberg@nih.gov
             /note-"Organ: kidney; Vector: pT/T3D-Pac (Pharmacia) with a modified polylinker; Site_1: No: I; Site_2: Eco RI; Plasmid DNA from the normalized library NCI_CGAP_Kid3 was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (cloneIDs 1322376-132391, 1456007-1456775, and 1500552-1502855). Subtraction by Bento Soares and M. Fatima Bonaldo. 75 g 145 t 5 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                         /clone="IMAGE:2496288"
/clone_lib="NCI_CGAP_Kid11"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                             /db_xref="taxon:
                                                                                                                                                                                                                                                                                                                                                    'organism="Homo sapiens"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Christopher Moskaluk, M.D., Ph.D.,
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Best Local Similarity 88. Matches 333; Conservative

15.5%;

Score 239; DB 63; Pred. No. 2.5e-47; Mismatches

Length 446; Indels

44;

Gaps

5

0

Query Match

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FEATURES
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AUTHORS
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                                                                                                                                                                                                    Email: estéwatson wustl.edu
Insert Size: 1454
High quality sequence stops: 372 Source: IMAGE Consortium, LLNI
This clone is available royalty-free through LLNI; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 1454 Std Error: 0.00
                                                                                                                                                                                                                                                                                                                                                                                                                                    Washington University Schu4444 Forest Park Parkway,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hillier, L., Lennon, G., Becker, M., Bonaldo, M.F., Chiapelli, B., Chissoe, S., Dietrich, N., DuBuque, T., Favello, A., Gish, W., Hawkins, M., Hultman, M., Kucaba, T., Lacy, M., Le, M., Le, N., Mardis, E., Moore, B., Morris, M., Parsons, J., Prange, C., Rifkin, L., Rohlfing, T., Schellenberg, K., Soares, M.B., Tan, F., Thierry-Meg, J., Trevaskis, E., Underwood, K., Wohldmann, P., Waterston, R., Wilson, R.
                                                                                                                                                                                                                                                                                                                                                                                 Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Wilson RK
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Location/Qualifiers
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/organism="Homo sapiens"
/db_xref="GDB:414189"
/db_xref="taxon:9606"
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   White, C. J., Lee, N.H., Kirkness, E.F., White, C., Sutton, G., Blake, J.A., Brown, G., Blake, G., Bla
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Brandon, R.C.,

Weinstock, K.G., Gocay

Gocayne, J.D.,

Fuldner, R.A.

Earle-Hughes, J.,

COMMENT

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422 aagatacacacgctttt 438
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Eukaryota; Métazoa; Chordata; Craniata; Vertek
Eutheria; Primates; Catarrhini; Hominidae; Hon
1 (bases 1 to 365)
Adams, M.D., Kerlavage, A.R., Fleischmann, R.D.,
                                                                                                                                            receptor
AA298563
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EST114178 HSC172 cells I Homo sapiens cDNA
receptor (IL13R), mRNA sequence,
                                                                     Homo sapiens
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//dev_stage="73 days post natal"
//lab_host="0H10B (ampicillin resistant)"
//lab_host="0"...hole hrain: Vector: Laimid Ba;
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                                                                                                                                                                                                                                                                                                                627 acattatgtctgggtacttcttggataccaattacaacttgttttactggtatgagggctt 686
                                                                                                                                                                                                                                                                                                                                                                                                           567 tggattgcgtatattacaattggcaatatttactctgttcttggaaacctggcataggtt
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                         agatttctatatttgtgttaatggatcatcagagaacaagcctgaaatatcaaggaatca 866
                                                                                                                                                                                                                   ggatcatgcattaaatatatttggaaacagtgtgttgattacatcaaggctgatggacaa
  AGATTTCTATATTTGTGTTAATGGATCATCAGAGANCAAGCCT
                                                                                                                                        aatataggatgcagatttccctatttggcaataaaggagcagtgaggcatcagactataa
                                                                                             AATATAGGATGCAGATTTCCCTATTTG------GAGGCATCAGACTATAA
                                                                                                                                                                                                                                                                                                                                                                                    TGGATTGCGTATATTACAATTGGCAATATTTACTCTGTTCTTGGAAACCTGGCATAGGT- 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    342;
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Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of cDNA sequence
Nature, 377 (6547 Suppl), 3-174 (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kelley,J.M., Kelley,J.C., Liu,L.-I., Marmaros,S.M., Merrick,J.M., Moreno-Palanques,R.F., McDonald,L.A., Nguyen,D.T., Pelligrino,S.M., Phillips,C.A., Ryder,S.E., Scott,J.L., Saudek,D.M., Shirley,R., Small,K.V., Spriggs,T.A., Utterback,T.R., Weldman,J.F., Li,Y., Bednarik,D.P., Cao,L., Cepeda,M.A., Coleman,T.A., Collins,E.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      For clone availability, additional sequence and expression information related to this EST, please check the TIGR Human Gene Index (http://www.tigr.org/tdb/hgi/hgi.html)
Seq primer: M13 Reverse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bioinformatics
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         On Sep 12, 1996 this sequence version replaced gi:1393411 Other_ESTs: THC194124
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Glodek,A., Gnehm,C.L., Hanna,M.
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/cell_type="fibroblast"
/cell_line="HSC172 (16PDL)"
/dev_stage="fetal"
/note="Organ: lung; Vector: pBluescript SK-;
ECORI; Site_2: XhOI"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Homo sapiens"
/db_xref="ATCC (inhost):178283"
/db_xref="taxon:9606"
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Pred. No. 5.3e-40;
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                                                                                373 CARACACCTACCCAAAATGGT
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                                                                                                                                                                                                                                                                            al Similarity
117; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: jwallace@u.washington.edu
Clones may be purchased from Research Genetics (info@resgen.com).
BAC end Web Server: http://www.htsc.washington.edu
Plate: 3132 row: D column: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Mahairas GG, Wallace JC,
High Throughput Sequencing Center
University of Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Manuaras,G.G., Wallace,J.C., Smith,K., Swartzell,S., Shaker,R., Schmidt,S., Traicoff,R. and Hood,L.E. Construction of a Characterized Clone Resource for Generation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A 7761600
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CNSC039G
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Location/Qualifiers
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Class: BAC ends
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Fax: (206) 616-3887
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished (1998)
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/clone="Plate=3132 Col=9 Row=D"
/clone_lib="CIT Approved Human Genomic Sperm Library D"
                                                                                                                                                                                                                                                                                                                                                                                                                              /sex="male"
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BP 191 91006 EVRY cedex - FRANCE (E-mail : seqrefégenoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP).

The BDGP is constructing a physical map of the Drosophila please see http://www.fruitfly.org The BDGP Drosophila please see http://www.fruitfly.org The BDGP Drosophila Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, Prosophila Drosophila Drosoph
                                                                                  KRDAADDRDDAATWTTWTTTTTRDTDDWKWKTDTWTRWAADRTWDRDDDDDRDRAGTAGR
                                                                                                                                                                                                                          tcagactataaagatttctatatttgtgttaatggatcatcagagaacaagcctgaaata 855
                                                                                                                                                                                                                                                                                              GDKDDDGKGKDADDDTDGTKDDDDKDKWDDWDKAKGTWGDATWAWAATDWWWWGWADADW
                                                                                                                                                                                                                                                                                                                             RKRKDKKDRKDGDDDKKGGKKKKAAKAAKWATKWWDDWDWDKDWKWDGAKDRKADDDDGA
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Similarity 15.6%; Pr
86; Conservative 253;
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Direct Submission
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fly) genomic survey sequence.
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64 c 131 g
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/clone="BACR08K10"
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/db_xref="taxon:7227"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AARAAWWAWW
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BACN15A12 of DrosBAC library from Drosophila melanogaster
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191 91006 EVRY cedex - FRANCE (E-mail : seqrefégenoscope.cns.fr
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/plasmid="pBeloBaCII"
/db_xref="taxon:7227"
/clone_lib="DrosBaC"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: msoares@blue.weeg.uiowa.edu
Oligo-dT track not found, Not I site shown in beginning of sequence
is likely internal to the message. cDNA Library Preparation: M.B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    451 Eckstein Medical Research Building Iowa City, Tel: 319 335 8250
Fax: 319 335 9565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  암
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                                  /lab_host="DHIOB" (Life Technologies)"
/note="vector: p773D-Pac (pharmacia) with a modified
/note="vector: p773D-Pac (pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: EoR; The UI-R-C3
library is a subtracted library of a series, ultimately
derived from a mixture of individually tagged normalized
libraries from rat placenta, adult lung, brain, liver,
kidney, heart, spleen, ovary, muscle, and 8, 12 and 18-day
embryos, after a series of subtractions to reduce the
representation of cDNAs from which ESTs had already been
generated. The following serially subtracted libraries
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1 to 160)
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/strain="Sprague-Dawley"
/db_xref="taxon:10116"
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/clone_lib="VI-R-C3"
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UI-R-E1. The tag is a
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              Web: www.genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part of collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk - This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CNSJ15FP 1201 bb DNA GSS 26-JUL-1999 Drogophila melanogaster genome survey sequence T7 end of BAC BACN15K18 of DrosBAC library from Drosophila melanogaster (fruit
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Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                  Submitted (23-JUL-1999) Genoscope - Centre BP 191 91006 EVRY cedex - FRANCE (E-mail :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LLY), genomic survey sequence.
PBeloBAC11
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/clone\_lib="DrosBAC" /clone="BACN15K18" /note="end : T7" a 171 c 199 g

357

197

/organism="Drosophila /plasmid="pBeloBAC11" /db\_xref="taxon:7227"

melanogaster"

Location/Qualifiers

ORIGIN

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RESULT 1
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TITLE
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Matches
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                                                                                                                                                                                                                                                                                      BP 191 91006 EVKI COURT

- Web: www.genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk - This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton oroject grant. The DNA was prepared from embryos by Alain Bucheton
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Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
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BACN37D10 of DrosBAC library from
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fx
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/clone="BACN37D10"
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/plasmid="pBeloBAC11"
/db_xref="taxon:7227"
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1,

Query Match

2.98;

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                                                                                                                                                                                                                                                              Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 acconstructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; on bw sp, the same strain used for the BDGP's pland EST libraries. A more detailed description of the library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TRKRWGAWWRADAWARDDTDGKDTRTADKDRKR 1058
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

1 (bases 1 to 1101)
                                                                                                                                                                         and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can I found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Direct Submission
Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fi
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                                                                                    /organism="Drosophila melanogaster"
/db_xref="taxon:7227"
/clone_lib="RPCI-98"
                                     /clone="BACR05D19"
/note="end : T7"
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23-OCT-1996; AU0668.
23-OCT-1995; AU-006135.
22-DEC-1995; AU-007276.
09-SEP-1996; AU-002208.
                                                                                                                DNA encoding animal haemopoietin receptor which interacts with interleukin-13 - useful to treat asthma, allergy or condition exacerbated by IgE production

Claim 5; Page 52-54; 93pp; English.

Novel mouse and human haemoprotein receptors (W09821 and W09822),

designated NR4, comprise the interleukin-13 (IL-13) receptor alpha-chain. The human NR4 amino acid sequence was deduced from a composite DNA sequence (T66165) derived from bone marrow cDNA clones. Recombinant NR4, or fusion proteins including NR4, can be produced in transformed host cells. The receptor molecules and their components are useful in the development of a range of
                    agonists, antagonists, therapeutics and diagnostic reagents based on ligand interaction with its receptor, esp. for the development of cpds. capable of modulating the activity of II-13 and related cytokines such as interleukin-4 for the treatment of allergy, asthma
                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB; T66165
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W09822;
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/label= Transmembrane_domain
367. 426
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/note= "Ig-like domain"
36
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/label= WSDWS_motif
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Bust Local Similarity 99.8%;
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                                                                                                                                                                                                                                                                                                                      .104
                                                                                                                                                                                                                                                                                                                                                                /label= Extracellular domain /note= "Ig-like domain" 36
                                                                                                                     343. .366
/note= "unidentified
                                                                                                                                                                                                                                                                    /label= N-glycosylation_site
119...342
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                                             /label= Cytoplasmic_tail
                                                                                            'label = Transmembrane_domain
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                                                                                                                                                                                                                                                                                                                                     'label= N-glycosylation site
                                                                                                                                                                                                                                                                                                                                                                                                                                                        /label= Mat_protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
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23-OCT-1995; AU-006135.
22-DEC-1995; AU-007276.
09-SEP-1996; AU-007208.
(AMRA-) AMRAD OPERATIONS PTY LTD.
Hilton DJ, Metcalf D, Nicola NA,
W58987 standard;
W58987;
11-SEP-1998 (fir
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Local Similarity 74.9%;
nes 319; Conservative 4
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                                                                                                                                                                              IVLLLYLKRLKIIIFPPIPDPGKIFKEMFGDQNDDTLHWKKYDIYEKQTKEETDSVVLIE 420
                                                                                                                                                                                                                                       GVLPDTLNTVRIRVKTNKLCYEDDKLWSNWSQEMSIGKKRNSTLYITMLLIVPVIVAGAI
                                                                                                                                                                                                                                                                                                  DDLYVQWENPQNFISRCLFYEVEVNNSQTETHNVFYVQEAKCENPEFERNVENTSCFMVP
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                                                                                                        NLKKAA
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                                                                                                                                                                IILLFYLKRLKIIIFPPIPDPGKIFKEMFGDQNDDTLHWKKYDIYEKQSKEETDSVVLIE
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                               Protein; 177
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       40;
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Mest Local S
Matches 177
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Homo sapien: .
W09814576-A2:
09-APR-1998.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         grewth, as an activator or inhibitor, or as a chemotactic or chemok: setic, haemostatic and thrombocytic, receptor/ligand, anti-inflammatory or tumour inhibitor agents.

Sequence 177 AA;
                                                                                                         18-MAR-1992; 108309.
11-SEP-1991; 508309.
11-SEP-1990; JP-240638.
(TAKA/) "PAKATSU K.
Takatsu K, Tominaga A, Takagi S,
WPI; 92-980329/12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ameliorating a medical condition in a mammal. Such compositions may be used for, e.g. research purposes as markers for tissues, majecular weight markers for gels, primers or probes, for nutrition as carbon, nitrogen or carbohydrate source. They can also be used as a cytokine for cell proliferation and differentiation activity, as immune stimulants or suppressors, e.g. for viral, bacterial or fungal infections, for autoimmune diseases such as multiple sclerosis or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nucleic acids encoding novel secreted proteins—usefu anti-inflammatory, immuno-stimulatory or suppressing at Disclosure; Page 81-82; 110pp; English.

The sequence is that of a secreted protein encoded by an isolated polynucleotide which may be of use in the production of therapeutic compositions for treating or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  autoimrine
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Agostino MJ, Jacobs K, Lavallie ER, Mccoy
Racie LA Spaulding V, Treacy M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
adult, place
                                            involving IL-5
Claim 7; Page 21-23;
                                                                                                                                                                                                                                                                R22211;
22-JUL-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13-OCT-1997; U18007,
94-OCT-1996; US-726237.
                                                                                                                                                                                                                                Autoimmune disorder;
                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                             R22211 standard; Protein; 415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-PSDB; V11622
                                                                            for treatment of auto-immune
                                                                                             Human and murine
                                                                                                                                                                                                     EP-475746-A.
                                                                                                                                                                                                                   jouse
The inventors claim: an is 
(secretcry) interleukin-5 
murine early, B cellomRNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             205 MYKDNAGKIKPSFNIVPLTSRVKPDPPHIKNLSFHNDDLYVQWENPQNFISRCLFYEVEV 264
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f
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消e、光光Sease; anti-inflammatory; immune; stimulation
                                                                                                                                                                                                                                interleukin 5 (II-5) receptor with signal peptide. disorder: therapy; eosinophilia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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uta; cDNA library; clone DA136_11; secreted pro
                                                                                                                                                                                                                                                              (first_entry)
                                                                                     interleukin-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%;
                                               65pp; English
 isolated cDNA sequence encoding murine
-5 (IL-5) receptor, which is synthesised
A; an isolated murine (secretory) IL-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 942;
Pred. No.
                                                                            -5 receptor and DNA encoding
and eosinophilia conditions
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3.7e-81;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                - useful
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Best Local S
Matches 97
            The inventors claim: an isolated cDNA sequence encoding murine (secretory) interleukin-5 (II-5) receptor, which is synthesised from murine early B cell mRNA; an isolated murine (secretory) II-5 receptor; an isolated cDNA sequence encoding human (secretory) II-5 receptor, which is synthesised from mRNA of human peripheral blood eosinophil; and an isolated human (secretory) II-5 receptor. Also claimed are a COS monkey cell transfected with a recombinant vector
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  receptor; an isolated cDNA sequence encoding human (secretory) II-5 receptor, which is synthesised from mRNA of human peripheral blood eosinophil; and an isolated human (secretory) II-5 receptor. Also claimed are a COS monkey cell transfected with a recombinant vector contg. the DNA; secretory human II-5 lacking a cytoplasmic and a transmembrane region; and an expression vector.
                                                                                                                                     Disclosure; Page 45; 65pp; English.
                                                                                                                                                                                                                          Takatsu K,
WPI; 92-09
                                                                                                                                                                                                                                                                                                                                                                                                                            22-JUL-1992 (first entry)
Sequence of interleukin 5 receptor (IL-5R.8).
                                                                                                                                                                                                        N-PSDB; Q22976
                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                             Autoimmune disorder; therapy;
                                                                                                                                                     nvolving IL-5
                                                                                                                                                                     Human and murine interleukin-5 for treatment of auto-immune au
                                                                                                                                                                                                                                                          (TAKA/) TAKATSU K.
                                                                                                                                                                                                                                                                        18-MAR-1992.
11-SEP-1991; 308309
11-SEP-1990; JP-2400
                                                                                                                                                                                                                                                                                                                            EP-475746-A.
                                                                                                                                                                                                                                                                                                                                                             peptide
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                                                                                                                                                                                                                      csu K, Tominaga A, Takagi S, Murata
92-090329/12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TRLFPPVPAPKSNIKDL------PVVTEYEKPSNETKIEVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PPVTNLSVSVENLCTVIWTWNP-PEGASSNCSLWYFSHF-GDKQDKKIAPETRRSIEVPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    --IFPPIPDPGKIFKEMFGDQNDDTLHWKKYDIYEKQTKEETDSVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NKLCYEDDKLWSNWSQEMSIGKKRNSTLYITMLLIVPVIVAGAIIVLLLYLKRLKII---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLFYEVEVNNSQTETHNVFYVQEAKCENPEFERNVENTSCFMVPGVLPDTLNTVRIRVKT 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VSLRCTWLVGKDAPEDTQYFLYYRFGVLTE--KCQEYSRDALNRNTACWFPRTFINSKGF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    l Similarity
97; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        415 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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secretory human
                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
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                                                                                                                                                                 -5 receptor and Drand eosinophilia
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Pred.
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No. 7.
lacking
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7.5e-22;
                                                                                                                                                                                     DNA encoding
a cytoplasmic
                                                                                                                                                                     conditions
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and
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isecretory) interleukin-5 (IL-5) receptor, which is synthesised from murine early B cell mRNA; an isolated murine (secretory) IL-5 receptor; an isolated cDNA sequence encoding human (secretory) IL-5 receptor, which is synthesised from mRNA of human peripheral blood eosinophil; and an isolated human (secretory) IL-5 receptor. Also claimed are a COS monkey cell transfected with a recombinant vector contg. the DNA; secretory human IL-5 lacking a cytoplasmic and a sequence 398 AA;
                                                                                                                                                                                                                                                                                    18-MAR-1992.
11-SEP-1991;
11-SEP-1990;
                                                                                                                                                                                                                                                    Takatsu K, Tominag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       transmembrane
Sequence 415
                                                                                                                                                                                                                                    Takatsu K, Tominaga A, Takagi S, WPI: 92-090329/12.
                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                      Human and murine interleukin-5 receptor and DNA encoding
                                                                                                                                                                                                                                                                                                                                   EP-475746-A.
                                                                                                                                                                                                                                                                                                                                                    Mouse
                                                                                                                                                                                                                                                                                                                                                                   Autoimmune
                                                                                                                                                                                                                                                                                                                                                                                22-JUL-1992 (first enti
Sequence of interleukin
                                                                                                                                                                                                                                                                                                                                                                                                                   R22212;
                                                                                                                                                                                                                                                                                                                                                                                                                                R22212 standard; Protein;
                                                                                                                                                                                                       for treatment of auto-immune and
                                                                                                                                                                                       nvolving IL-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              365 TRLFPPVPAPKSNIKDL------PVVTEYEKPSNETKIEVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        374 -- IFPPTPDPGKIFKEMFGDQNDDTLHWKKYDIYEKQTKEETDSVV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NKLCYEDDKLWSNWSQEMSIGKKRNSTLYITMLLIVPVIVAGAIIVLLLYLKRLKII---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLFYEVEVNNSQTETHNVFYVQEAKCENPEFERNVENTSCFMVPGVLPDTLNTVRIRVKT 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VSLRCTWLVGKDAPEDTQYFLYYRFGVLTE--KCQEYSRDALNRNTACWFPRTFINSKGF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EQHSVQIMVKDNAGKIKPSFNIVPLTSRVKPDPPHIKNLSFHNDDLYVQWENPQN-FISR 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HEGFAASVRTILKSSHTTLASSWVSAELKAPPGSPGTSVTNLTCTTHTVVSSHTHLRPYQ 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                    disorder;
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                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                     JP-240638.
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23.9%;
                                                                                                                                                                                                                                                                                                                                                                therapy;
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                                                                                                                                                                                                                                                       Murata
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.5e-22
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Matches Query Match Eest Local

l Similarity 97; Conser

Conservative

74;

Mismatches

179;

Gaps

14;

90

13.7%;

Score 318; DB 1 Pred. No. 7e-22;

DB 1;

Length

33 PPVTNLSVSVENLCTVIWTWNP-PEGASSNCSLWYFSHF-GDKQDKKIAPETRRSIEVPL

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WARSOLD TO SOLUTION OF SOLUTIO
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                                                                                                              testis tissue obtained from a Celebus macaque. The resulting polypeptide is a receptor for cytokines (particularly interleukin-13) and is expressed on the surface of testicular cells, probably being involved in spermatogenesis. It can be used to detect ligands promoting proliferation and/or differentiation of such cells in cultures and may also be used to treat infertility. Antagonists of this receptor may be used to characterise ligand-receptor interactions and as male-specific contraceptives. By blocking the action of II-13, receptor antagonists and ligand-binding this receptor can also be used to modulate immune function, e.g. in allergy and asthma, as a diagnostic to determine circulating levels of ligand and also to isolate and purify ligands.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30-MAR-1998 (first entry)
Celebus macaque Ecytor2 protein.
Cytokine receptor; ligand binding; testicular cell; spermatogenesis;
infertility; antagonist; contraceptive; diagnostic; therapeutic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New nucleic acid encoding testis-specific cytokine receptor for identification of ligands or antagonists, potentially for male contraceptives or for infertility treatment Example 4: Page 56-57; 79pp; English.
   express the receptor, 
Sequence 372 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This sequence represents a novel ligand-binding receptor, Zcytor2, which shares homology with cytokine receptors and is isolated from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-PSDB; T96784
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (ZYMO) ZYMOGENETICS INC. Baumgartner JW, Farrah TM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18-SEP-1997.
12-MAR-1997; U04043.
13-MAR-1996; US-013345.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      W36616 standard; Protein;
                                                            Antibodies can be used to assay circulating receptor (an abnormal level may be indicative of disease such as cancer), for labelling cells that
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Macaque sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    348
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83

92 32

ERICLOV----GSQCSTNESEKPSILVEKCIS----PPEGDPESAVTELQCIWHNL---

PPV-NFTIKVTGLAQVLLQWKPNPDQEQRNVNLEY

-QVKINAPK-EDDYETRIT

82

ESKCVTIL::KGFSASVRTILQNDHSLLASSWASAELHAPPGSPGTSIVNLTCTTNTTEDN

Matches Query Match

102;

Similarity

12.8%; ilarity 24.8%; Conservative (

65;

Score 296.5; DE Pred. No. 8.1e-2 55; Mismatches 1

BB 1; --20;

180;

Indels Length

65;

Gaps

16;

33 PPVTNLSVSVENLCTVIWTWNP-PEGASSNCSLWYFSHFGDKQDKKIAPETRRSIEVPLN 91

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 Query Match
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06-DEC-1991; 120521.

27-DEC-1990; EP-811030.

27-70-1991; EP-810327.
                       encoding it, for treatment of interleukin-5 mediated disorders such as chronic asthma
Claim 7; Fig 1; 15pp; English.
This maino acid sequence was deduced from the nucleotide sequence,
Excluted as detailed in Q25790. The cytoplasmic domain is 58 amino
acids long. A domain implicated in signal transduction processes
can not be found in this short cytoplasmic tail. Recombinant IL-5
alpha chain can be used as an IL-5 antagonist in chronic asthma or
other disease states with demonstrated esosinophilia. It may also be
used either alone or with the beta chain of the whole IL-5 receptor
                                                                                                                                                                                                (HOFF) HOWEMANN LA ROCHE'S Devos R, Fiers W, Plaetinck WPI; 92-218502/27.
                                                                                                                                                                                                                                                                                                                                             Interleukin-5; chronic ast
Sequence
                                                                                                                                                       Recombinant alpha chain of human interleukin-5 mee
                                                                                                                                                                                                                                                                                                                               screeniny antagonists;
              as a tool
                                                                                                                                                                                     N-PSDE; 025790
                                                                                                                                                                                                                                                                                                     EP-492214
                                                                                                                                                                                                                                                                                                                 Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WSEWSDKQCWEVEELLKKTL---LLFLLPF---GFILILVIFVTGL
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for screening for IL-5
421 AA;
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Pred. No. 2e-20;
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Tavernier
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Sequence

380 AA;

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RESULT
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        The present sequence represents the human interleukin-13 (IL-13) binding chain of the interleukin-13 receptor, designated IL-13bc. IL-13bc acts a mediator of the known biological activities of IL-13. Recombinant IL-13bc proteins, and antibodies raised against them, are used to inhibit the binding of IL-13 to its receptor. They are particularly used to treat IgE-mediated conditions, e.g. allergy, asthma and immune complex disorders, especially lupus, nephritis, thyroiditis and Grave's disease. They are also used to treat immune deficiency (particularly in haematopoietic progenitor cells), cancer etc., and to increase macrophage activation, e.g. in vaccination. To potentiate IL-13 activity, a protein with such activity is combined with IL-13bc and the mixture applied, in vivo, to a cell expressing at least one chain of the IL-13 receptor other than IL-13bc. IL-13bc can also be used in diagnosis to detect expression of IL-13b. its receptor or binding chain, and to raise specific
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                27-MAR-1998 (first entry)
27-MAR-1998 (first entry)
Human II-13 binding chain of the II-13 receptor.
Interleukin-13; II-13; interleukin-13 receptor b
Interleukin-13; receptor binding inhibition; Igf
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W35295
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war: 97-448632/41.
                                                                                                                                                                                                                                                                                                                                                                                     01-MAR-1996; US-609572.
(GEMY) GENETICS INST II
Collins M, Donaldson D,
                                                                                                                                                                                                                                                                                       treating immunoglobulin
                                                                                                                                                                                                                                                                                                   New nucleic acid encoding interleukin-13 receptor binding chain transformed cells - proteins, antibodies and inhibitors, for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Domain
                                                                                                                                                                                                                                                   Claim 11; Pages 34-35; 49pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                        28-FEB-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                --RLKIIIFPPIPDPGKIFKEMFGDQNDDTLHWKKYDIYEKQTKEETDSVVL 418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PVSAFPIHCFDYEVKIHNTRNG-----YLQIEKLMTNAFISIIDDLSKY-------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TFILSKGRDWLSVLVNGSSKHSAIRPFDQLFALHAIDQINPPLNVTAEIEGTRLSIQWEK 260
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  standard;
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may be useful for
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/note- "putative"
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some tumours
                                                                                                                                                                                                                                                                                     e.g. Graves
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                                                                                                                                                                                                                                                                                     disease
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                          New nucleic acid encoding testis-specific cytokine receptor - useful for identification of ligands or antagonists, potentially for use as male contraceptives or for infertility treatment claim 2; Page 47-48; 79pp; English.

This sequence represents a novel ligand-binding receptor, Zcytor2, which shares homology with cytokine receptors and was isolated from placental polyA+ RNA. The resulting polypeptide is a receptor for cytokines (particularly interleukin-13) and is expressed on the surfort testicular cells, probably being involved in spermatogenesis. It
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human Zcytor? cytokine receptor protein. Cytokine receptor; ligand Minding; testi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          W36613 standard; Protein; 380
W36613;
                                                                                                                                                                                          N-PSDB; T96782
                                                                                                                                                                                                                         OHara PJ;
                                                                                                                                                                                                                                                                                                                     WO9733913-A1.
                                                                                                                                                                                                                                                                                                                                                  Domain
                                                                                                                                                                                                                                                                                                                                                                                 Domain
                           be used to detect ligands that promote proliferation and/or
                                                                                                                                                                                                                                      Baumgartner
                                                                                                                                                                                                                                                                  12-MAR-1997; U04043.
13-MAR-1996; US-013345
                                                                                                                                                                                                                                                                                                                                                                                                                               rey
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                                                                                                                                                                                                                                                                                                    18-SEP-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                           infertility; antagonist;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HIKNLSFHND---DLYVQWENPQNFI-SRCLFYEVEVNNSQTETHNVFYVQEAKCENPEF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C-ENIFREGOYFGCSFDLTKVKDSSFEOHSVQIMVKDNAGKIKPSFNIVPLTSRVKPDPP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LWALLLCAGGGGGGGAAPTETOPPVTNLSVSVENLCTVIWTWNPPEGAS--SNCSLWYF 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ETTYWIS-PQGIPETKVQDMDCVYYNWQYLLCSWKPGIGVLLDTNYNLFYWYEGLDHALQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SHFGDKQDKKIAPETRRSI------EVPLNERICLQVGS----QCSTNESEKPSILV 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               107;
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                                                                                                                                                                                                                                      ETICS INC.
Farrah TM,
                                                                                                                                                                                                                                                                                                                                                /label-
25. .339
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26.0%;
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contraceptive;
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Pred. No. 8.
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cultures
receptor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           testicular cell;
tive; diagnostic;
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may also be used to treat
be used to characterise
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                                                                                             was isolated from human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            spermatogenesis; therapeutic.
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                                                              surface
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Best Local S
Matches 107
                                                                               17-DEC-1997: 303815.
04-JUN-1997: 303815.
12-JUN-1996: US-017843.
(HUMA-) HUMAN GENOME SCI INC.
(SMIK ) SMITHKLINE BEECHAM CORP.
APPELbaum ER, HU J;
WPI: 98-034974/04.
   Claim 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ligand-receptor interactions and as male-specific contraceptives. By blocking the action of IL-13, receptor antagonists and ligand-binding this receptor can also be used to modulate immune function, e.g. in allergy and asthma, as a diagnostic to determine circulating levels of ligand and also to isolate and purify ligands. Antibodies can be used to assay circulating receptor (an abnormal level may be indicative of disease such as cancer), for labelling cells that express the receptor,
                                                                                                                                                                                                                                                                                                                                Human cytokine/peptide receptor, HR-1 receptor.
HR-1 receptor; cytokine receptor; peptide hormone receptor;
infection; burn; trauma; asthma; allergy; AIDS; aplastic and
                                                                                                                                                                                                                                                                                                                                                                                                                    W41502 standard; Protein; 380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                  N-PSDB; V04075
                                                                                                                                                                                           EP-812913-A2.
                                                                                                                                                                                                                                         Protein
                                                                                                                                                                                                                                                                                                        Homo sapiens.
                                                                                                                                                                                                                                                                                                                           neutropaenia;
                                                                                                                                                                                                                                                                                                                                                                                      08-JUN-1998 (first entry)
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                                  ncrease resistance
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ERNVENTS --- CEMVPGVLPDTLNTVRIRVKINKLCYEDDKLWSNWSQEM -----SIGKK 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HIKNLSFHND---DLYVQWENPQNFI-SRCLFYEVEVNNSQTETHNVFYVQEAKCENPEF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             --VYLTFTRESSCEIKLKWSIPLGPIPARCFDYEIEIREDDTT-----LVTATVENETY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CVDYIKADGQNIGCRFPYLEASD--YKDFYICVNGSSENKPIRSSYFTFQLQNIVKPLPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C-ENIFREGQYFGCSFDLTKVKDSSFEQHSVQIMVKDNAGKIKPSFNIVPLTSRVKPDPP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EKC -- ISPPEGDPESAVTELQCIWHNLSYMKCSWLPGRNTSPDTNYTLYYWHRSLEKIHQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SHFGDKQDKKIAPETRRSI-----EVPLNERICLQVGS----QCSTNESEKPSILV
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                                 cytokine/peptide
ase resistance to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  al Similarity
107; Conserv
   Page
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                       therapy
   27-28;
                                                                                                                                                                                                        /label= Mat_protein
/note= "Claim 14"
                                                                                                                                                                                                                         /label-
                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                        /label= Sig_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12.7%;
                                                                                                                                                                                                                                         .380
34pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -GFILILVIEVTGL--LLRKPNTYP-KMIPEFFCD
                                 hormone receptor, HR-1 receptor - useful to infections in individuals with trauma and/or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   63;
   English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ----RSKVNIYC-SDDGIWSEWSDKQCWEGEDLSKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 295.5; DB:
Pred. No. 8.6e-20;
3; Mismatches 169
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
. Fest Local Similarity
Natches 107; Conserv
(8-DEC-1997.
09-JUL-1996;
12-JUN-1996;
                                                                                                                                                             Cytokine: hormone receptor; AIDS; acquired immune deficienc syndrome; aplastic anaemia; neutropaenia; cancer treatment; infection resistance; diagnosis; tumours; HR-1 receptor;
                                                                                                                                                                                                                               w33603;
08-JUN-1998 (first entry)
                                                      109747742-A1
                                                                                                            Key
                                                                                                                                               asthma; allergic; haematopoietic;
                                                                                                                                                                                                                                                                               W33603
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ERNVENTS----CFMVPGVLPDTLNTVRIRVKTNKLCYEDDKLWSNWSQEM-----SIGKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CVDYIKADGONIGCREPYLEASD--YKDFYICVNGSSENKPIRSSYFTFQLQNIVKPLPP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EKC--ISPPEGDPESAVTELQCIWHNLSYMKCSWLPGRNTSPDTNYTLYYWHRSLEKIHQ 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -- VYLTFTRESSCEIKLKWSIPLGPIPARCEDYEIEIREDDTT-----LVTATVENETY
                                                                                                                                                                                                                                                                               standard; Protein;
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U11459.
WO-U10262
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26.0%;
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                                                                     "signal peptide'
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Pred. No. 8.6e-20;
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RESULT 14
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Claim 15; Fig 1; 75pp; English.

Claim 16; F
12-JUN-1997.
07-NOV-1996; F01756.
06-DEC-1995; FR-014424.
(SNFI ) SANOFI SA.
Caput D, Ferrara P, Laurent P
WPI; 97-319773/29.
                                                                                                                                                                                                        Homo sapiens. W09720926-A1.
                                                                                                                                                                                                                                                         Interleukin-13 receptor; diagnosis;
                                                                                                                                                                                                                                                                                                    22-JUN-1998 (first entry)
Human interleukin-13 beta
                                                                                                                                                                                                                                                                                                                                                                                                   W24972 standard; protein; 380
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WPI; 98-052300/05
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(HUMA-) HUMAN GENOME SCI IN
(SMIK.) SMITHKLINE BEECHAM
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107; Conserv
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Pred. No. 8.6e-20;
Mismatches 169;
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RESULT 15
W41520
ID W41520
AC W41520
DT 22-JUN
DE Human 1
KW HR-1 rr
KW haematc
OS Homo si
FH Key
FT Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CC invention relates to new purified peptides comprising 380 or 427 amino CC and 427 as proteins are designated II-13R beta and alpha respectively. CC affinity, but acquires high affinity for II-13 while II-13R beta has high affinity for II-13 while II-13R has low CC receptor. Nucleic acids encoding II-13R beta and alpha are used as CC diagnostic probes to identify aberrant synthesis or genetic anomalies such as loss of heterozygosity and rearrangements, or chromosomal CC anomalies. They are also used for production of recombinant II-13R beta and alpha which can be used as II-13 antagonists, specifically to CC allergy. II-13 receptors are also useful as antisense molecules for gene CC allergy. II-13 receptors are also useful as antisense molecules for gene CC immunoassays) to diagnose diseases associated with abnormal expression CC of II-13 receptors; when coupled to a toxin also for treatment of used to identify ligands and modulators of II-13R. Nat the surface are cused to identify ligands and modulators of II-13R. Nat the surface are is sencoded by the nucleic acid sequence shown in Figure 2a in the CC sequence listing (T85828).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Bert Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Metches
                     Human HR-1 receptor. human; cytokine; infection; har a receptor; human; cytokine; infection; haematopoietic disorder; tumour; therapy; disomo sapiens.
       Peptide
                                                                                                                             22-JUN-1998 (first entry)
                                                                                                                                                                         W41520 standard; Protein;
                                                                                                                                                              W41520
                                                                                                                                                                                                                                                                                        340 TLLREWLPF-----
                                                                                                                                                                                                                                                                                                                     340 RNSTLYITMLLIVPVIVAGAIIVLLLYLKRLKIIIFPPIPDPGKIFKEMFGD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB; T85826, T86464.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            acids, useful for diagnosis
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                                                                                                                                                                                                                                                                                                                                                                                                            ERNVENTS---CFMYPGVLPDTLNTVRIRVKTNKLCYEDDKLWSNWSQEM-----SIGKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                      --VYLTETRESSCEIKLKWSIPLGPIPARCFDYEIEIREDDTT----LVTATVENETY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HIKNLSFHND---DLYVQWENPQNFI-SRCLFYEVEVNNSQTETHNVFYVQEAKCENPEF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CVDYIKADGQNIGCRFPYLEASD--YKDFYICVNGSSENKPIRSSYFTFQLQNIVKPLPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C-ENIFREGOYFGCSFDLTKVKDSSFEQHSVQIMVKDNAGKIKDSFNIVPLTSRVKPDPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ETTYWIS-POGIPETKYQDMDCYYYNWQYLLCSWKPGIGVLLDTNYNLFYWYEGLDHALQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EKC--ISPPEGDPESAVTELQCIWHNLSYMKCSWLPGRNTSDDTNYTLYYWHRSLEKIHQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SHFGDKQDKKIAPETRRSI-----EVPLNERICLQVGS----QCSTNESEKPSILV 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LYTFLISTTFGCTSSSDTEIKVNPPQDFEIVDPGYLGYLYLQWQPPLSLDHFKECTVEY-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      107;
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Location/Qualifiers
1. .21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 295.5; DB 1; Pred. No. 8.6e-20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            and treatment
                                                        therapy; diagnosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             beta receptor.
rising 380 or 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        73;
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N-PSDB; V04131.

Nucleic acid sequence encoding human cytokine peptide hormone receptor - useful to treat, prevent or diagnose, e.g. lowered resistance to infection, asthma, allergy or haematopoietic disease claim 13; Page 62-64; 76pp; English.
                                                                                                           compounds which bind to, and activate or inhibit, it. HR-1 receptor activators and agonists can be seed to treat, prevent or diagnose predisposition to lowered resistance to infection, asthma allergic or haematopoletic disorders, e.g. where induced by AIDS, applastic anaemia, neutropaemia or cytotoxic treatments for cancer
                                                                                                                                                                                                         and 52% similarity to the interleukin-5 receptor. Its amino acid sequence was deduced from a cDNA clone (see V04131) obtained from a human testis library. Recombinant HR-1 receptor can be expressed in claimed host cells, and used in a claimed method for identifying compounds which bind to, and activate or inhibit, it. HR-1
              HR-1 antagonists, e.g. antibodies of HR-1 receptor fragments, can be used to treat conditions associated with HR-1 receptor overexpression. The antibodies can also be used to determine HR-1 receptor levels, since overexpression may be diagnostic of tumours
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO9747741-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (HUMA-) HUMAN GENOME SCI INC.
(SMIK ) SMITHKLINE BEECHAM CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ppelbaum ER,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    l2-JUN-1996; U10262.
l2-JUN-1996; WO-U10262.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        98-052308/05.
                                                                                                                                                                                                                                                                                                                                    designated the HR-1 receptor,
380 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hu J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /label= Sig_peptide
22. .380
/label= Mat_protein
                                                                                                                                                                                                                                                                                                        receptor. Its amino
                                                                                                                                                                                                                                                                                                                                    identity
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Ş 밁 ş 밁 밁 ş 밁 Ş Query Match Best Local S Matches 107 232 HIKNLSFHND----DLYVQWENPQNFI-SRCLFYEVEVNNSQTETHNVFYVQEAKCENPEF 184 CVDYIKADGQNIGCRFPYLEASD--YKDFYICVNGSSENKPIRSSYFTFQLQNIVKPLPP 173 C-ENIFREGOYFGCSFDLTKVKDSSFEOHSVOIMVKDNAGKIKPSFNIVPLTSRVKPDPP Local Similarity 26.0 nes 107; Conservative 70 ----ELKYRNIGSETWKTIITKNLHYKDGFDLNKGIEAKIHTLLPWQC-TNGSEVQSSWA 124 10 LWALLLCAGGGGGGGAAPTETQPPVTNLSVSVENLCTVIWTWNPPEGAS--SNCSLWYF 67 ETTYWIS-PQGIPETKVQDMDCVYYNWQYLLCSWKPGIGVLLDTNYNLFYWYEGLDHALQ EKC--ISPPEGDPESAVTELQCIWHNLSYMKCSWLPGRNTSPDTNYTLYYWHRSLEKIHQ 172 SHFGDKQDKKIAPETRRSI------EVPLNERICLQVGS----QCSTNESEKPSILV 114 LYTFLISTTFGCTSSSDTEIKVNPPQDFEIVDPGYLGYLYLQWQPPLSLDHFKECTVEY- 70 12.7%; Score 295.5; DB 1; 26.0%; Pred. No. 8.6e-20; tive 63; Mismatches 169; Length 380; 73; Gaps 241 231 183 11 20;

Search completed: January 19, 2000, 20:00:53 Job time: 8948 sec

B 8 B 8

340 RNSTLYITMLLIVPVIVAGAIIVLLLYLKRLKIIIFPPIPDPGKIFKEMFGD 391

-GFILILVIFVTGL--LLRKPNTYP-KMIPEFFCD 379

294 TLKTTNETRQLCFVV------RSKVNIYC-SDDGIWSEWSDKQCWEGEDLSKK 339

--VYLTFTRESSCEIKLKWSIPLGPIPARCFDYEIEIREDDTT-----LVTATVENETY 293
ERNVENTS---CFMVPGVLPDTLNTVRIRVKTNKLCYEDDKLWSNWSQEM-----SIGKK 339

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#### Title: Perfect score: Sequence: Number of hits that pass the threshold : Word size : Database : Searched: Scoring table: OM protein - protein search, using sw model Run on: BLOSUM62 US-09-077-817-4 2324 1 MEMPARLCGLWALLLCAGGG.....QTKEETDSVVLIENLKKASQ 427 January 19, 2000, 14:58:48; Search time 71.05 Seconds (without alignments) 283.481 Million cell updates/sec PIR\_62:\* 142080 seqs, 47169319 residues 0 GenCore version 4.5 Copyright (c) 1993 - 1998 Compugen Ltd. pir1: \* pir2: \* pir3: \* pir4: \* 142080

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	BB	ID	
ы	318	13.7		2	123	erl
2	94	12.7	420	2	S21052	rleukin-5 rec
w	283.5	12.2	396	N	210	-5 rec
4	23	9.9	333	N	S21053	-5 rec
ر. ن	229	٠	335	N	402	ģ
Q	228		400	N	S06945	-ma
7	0	8.9	373	N	A55718	•
œ	205.5		369	N	149280	N
9	0	٠	369	N	A42565	N
10	197.5	•	831	N	JQ1655	õ
11	190	•	610	N	A34631	p H
12	189	•	610	N	A36116	3
13	189		412	2	A41070	
14	189	8.1	310	N	A29884	ín
15	186	٠	581	N	145971	
16	185	8.0	616	N	A30304	prolactin receptor
17	183	7.9	292	N	177525	ä
18	180	7.7	303	Ν	177524	prolactin receptor
19	180	7.7	608	N	I53269	in
20	176	7.6	630	Ν	151086	prolactin receptor
21		7.4	816	N	A36337	membrane glycoprot
22	172.5	7.4	622	N	A40144	-
23	170	7.3	897	$\vdash$	A39255	
24	0		396	N	S22909	interleukin-3 rece
25	16		830	N	I50455	prolactin receptor
26	٠	٠		N	S13684	granulocyte-macrop
27		٠	1092	N	JX0312	differentiation-st
28	-	6.9	719	ν	JC2181	differentiation-st
29	ı		378	N	A40266	interleukin-3 rece
30	125		896	ب	A35782	cytokine receptor
31		•	378	N	S50040	granulocyte-macrop
32	54.	٠	896	N	I56563	interleukin-3 rece
ω	149	6.4	878	۳	A40091	w
34	146.5	6.ω	808	N	S32823	somatotropin recep
35	145	6.2	638	N	A33991	somatotropin recep

interleukin-5 receptor alpha chain precursor (clone lambda h5R.12), membrane-anchored C;Speciaes: Homo sapiens (man) C;Date: 22-Nov-1993 #sequence\_revision 10-Nov-1995 #text\_change 20-Feb-1998 C;Accession: S21052; A46175 R;Murata, Y.; Takaki, S.; Migita, M.; Kikuchi, Y.; Tominaga, A.; Takatsu, K.

S21052

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	A32694	S50039	S33339	ZUHUR	B28176	S12136	149699	A44257	S17308	S04530	
	interferon alpha r	granulocyte-macrop	somatotropin recep	erythropoietin rec	somatotropin recep	somatotropin recep	glycoprotein 130 -	interleukin-6 sign	leukemia inhibitor	somatotropin recep	

## ALIGNMENTS

ON 374IPPPIDDPGKIPKEMFGDQNDDTLHWKKYDIYBKQTKBETDSVV 417	C:Bate: 21-Nov-1993 **sequence_revision 10-Nov-1995 **text_Change 20-Mar-1998 C:C.Accession: \$12357   R:Takaki S:; Tominaga, A:; Hitoshi, Y:; Mita, S:; Sonoda, E:; Yamaguchi, N:; Takatsu & Molecular cloning and expression of the murine interleukin-5 receptor. A:; Reference number: \$12357; MUID:91092260   A:; Residues: 1-415 crake A:; Residues: 1-415 cr
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65;

Gaps

16;

transmembrane

#status

predicte

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C;Accession: S21050; S78106
R;Murata, Y.; Takaki, S.; Migita, M.; Kikuchi, J. Exp. Med. 175, 341-351, 1992
A;Title: Molecular cloning and expression of th A;Reference number: S21050; MUID:92121815
                                                     A; Molecule type: DNA
A; Residues: 1-396 < MI
                                                                                                                                                                                                                                 C:Species: Homo sapiens (man)
C:Date: 29-Jan-1998 #sequence_revision
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               J. Exp. Med. 175, 341-351, A; Title: Molecular cloning A; Reference number: S21050;
                                                                                                  A; Accession: S21050
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: EMBL:X61176; NID:g33843; PID:
A;Experimental source: clone lambda h5R.12
R;Tavernfer, J; Tuypens, T; Plaetlnck, G; Verh
Proc. Natl Acad. Sci. U.S.A. 89, 7041-7045, 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Title: Molecular basis of the membrane-anchored A;Reference number: A46175; MUID:92357767 A;Accession: A46175
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                                                                                                                                                                                                                                                                               interleukin-5 receptor alpha chain precursor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Experimental source: HL-60 cells and eosinophils
A; Note: sequence extracted from NCBI backbone (NCBIN:116243, NCBIP:116244)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Residues: 1-420 <MUR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
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Best Local
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Residues: 333-420 <TAV>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           YSRLRSYQVSLHCTWLVGTDAPEDTQYFLYYRYGSWTE--ECQEYSKDTLGRNIACWFPR 200
                                                                                                                                                                                                                                                                                                                                                                                                ICHLWIKLEPPIPAPKSNIKDLEVTTN---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TVRIRVKTNKLCYEDDKLWSNWSQEMSIGKKRNSTLYITMLLIVPVIVAGAIIVLLLYLK 368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TFILSKGRDWLAVLVNGSSKHSAIRPFDQLFALHAIDQINPPLNVTAEIEGTRLSIQWEK 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PPVTNLSVSVENLCTVIWTWNP-PEGASSNCSLWYFSHFGDKQDKKIAPETRRSIEVPLN 91
                                                                                                                                                                                                                                                                                                                                                                                                                                        --RLKIIIFPPIPDPGKIFKEMFGDQNDDTLHWKKYDIYEKQTKEETDSVVL 418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DVQVRAAVSSMCREAG-LWSEWSQPIYVGNDEHKPLREWFVIVIMATICFILLILSLICK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PVSAFPIHCFDYEVKIHNTRNG-----YLQIEKLMTNAFISIIDDLSKY--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PQN-FISRCLFYEVEVNNSQTETHNVFYVQEAKCENPEFERNVENTSCFMVPGVLPDTLN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TKVKDSSFEQHSVQIMVKDNAGKIKPSFNIVPLTSRVKPDPPHIKNLSFHNDDLYVQWEN 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ----SY---MKCSWLPGRNTSPDTNYTLYYWHRSLEKIHQCENIFRE--GQYFGCSFDL 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ESKCVTILHKGFSASVRTILQNDHSLLASSWASAELHAPPGSPGTSVVNLTCTTNTTEDN 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ERICLOV-----GSQCSTNESEKPSILVEKCIS----PPEGDPESAVTELQCIWHNL---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PPV-NFTIKVTGLAQVLLQWKPNPDQEQRNVNLEY-----QVKINAPK-EDDYETRIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    102;
                                                 1-396 <MUR>
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         source:
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         EMBL:X61177; NID:g33839; ce: clone lambda h5R.27
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g and expression of
0; MUID:92121815
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No. 1.1e-15;
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                              PID: 933840
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PID: 933844
                                                                                                                                                                                      Y.;
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                                                                                                                                                                                      Tominaga,
                                                                                                                                                                                                                                                                                  lambda h5R.27) -
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                                                                                                                                          interleukin
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                                                                                                                                                                                      Α.;
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F;1-20/Domain: signal sequence #status predicted <SIG>F;?1-33/Product: interleukin-5 receptor #status predicted <MAT>F;35,131,137,142,216,244/Binding site: carbohydrate (Asn) (coval
                                                                   A;Molecule type: mrNA
A;Residues: 1-128,'r','130-333 <MUW>
A;Cross-references: EMBL:X62156; NID:g36465; PID:g36466
C;Krywords: alternative splicing; cytokine receptor; g1:
                                                                                                                                                          A Peference number: A; Accession: S78107
                                                                                                                                                                                    submitted to the EMBL Data A Peference number: S78107
                                                                                                                                                                                                                                                                                                                                          A;Title: Molecular cloning and expression A;Reference number: $21050; MUID:92121815 A;Accession: $21053
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C:Species: Homo sapiens (man)
C:Date: 29-Jan-1998 #sequence_revision 06-Feb-1998
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submitted to the EMBL Data Library, July
A;Reference number: 878106
                                                                                                                                                                                                                                   R, Murata,
                                                                                                                                                                                                                                                        A; Experimental source: clone lambda h5R.25
                                                                                                                                                                                                                                                                                                     A: Residues: 1-333 <MU
                                                                                                                                                                                                                                                                                                                                                                                                                                      R; Murata,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: DNA
A; Residues: 1-128, 'I', 130-396 <MUW>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            interleukin-5 receptor precursor,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cross-references: EMBL:X61177; NID:g33839; PID:g33840; Keywords: alternative splicing; cytokine receptor; gl: 1-20/Domain: signal sequence #status predicted <SIG>
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Accession: S21053; S78107
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TVRIRVKTNKLCYEDDKLWSNWSQEMSIGKKRNSTLYITMLLIVPVIVAGAIIVLLLYLK 368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PVSAFPIHCFDYEVKIHNTRNG-----YLQIEKLMTNAFISIIDDLSKY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TKVKDSSFEQHSVQIMVKDNAGKIKPSFNIVPLTSRVKPDPPHIKNLSFHNDDLYVQWEN 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ESKCVTILHKGFSASVRTILQNDHSLLASSWASAELHAPPGSPGTSVVNLTCTTNTTEDN 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ERICLQV-----GSQCSTNESEKPSILVEKCIS----PPEGDPESAVTELQCIWHNL--- 140
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ----SY---MKCSWLPGRNTSPDTNYTLYYWHRSLEKIHQCENIFRE--GQYFGCSFDL 189
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Pred. No. 7.7e-15;
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20-Feb-1998

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A; Molecule type: mRNA
A; Residues: 1-335 <TAV>
A; Cross-references: GB: M75914;
C; Keywords: cytokine receptor;
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A;Title: A human high affinity interleukin-5 receptor (IL5R) is composed of an, IL5-spec A;Reference number: A40267; MUID:92005669
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C:Species: Homo sapiens (man)
C:Date: 17-Jan-1992 *sequence_revision
C:Accession: A40267
R:Tavernier, J.: Devos, R.: Cornelis, S
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Best Local Similarity
Matches 82; Conserv
  261
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         309 TVRIRVKTNKLCYEDDKLWSNWSQEMSIGK 338
                                                                                                                                                                                                                                83
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             33 PPVTNLSVSVENLCTVIWTWNP-PEGASSNCSLWYFSHFGDKQDKKIAPETRRSIEVPLN 91
                                                                                                                                                                                                                                                                                                                                              PPVTNLSVSVENLCTVIWTWNP-PEGASSNCSLWYFSHFGDKQDKKIAPETRRSIEVPLN
                                    PQN-FISRCLFYEVEVNNSQTETHNVFYVQEAKCENPEFERNVENTSCFMVPGVLPDTLN 308
                                                                        TFILSKGRDWLSVLVNGSSKHSAIRPFDQLFALHAIDQINPPLNVTAEIEGTRLSIQWEK
                                                                                                              TKVKDSSFEQHSVQIMVKDNAGKIKPSFNIVPLTSRVKPDPPHIKNLSFHNDDLYVQWEN 249
                                                                                                                                                    YSRLRSYQVSLHCTWLVGTDAPEDTQYFLYYRYGSWTE--ECQEYSKDTLGRNIACWFPR
                                                                                                                                                                                                                                                                    ERICLQV-----GSQCSTNESEKPSILVEKCIS----PPEGDPESAVTELQCIWHNL---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PVSAFPIHCFDYEVKIHNTRNG-----YLQIEKLMTNAFISIIDDLSKY-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PQN-FISRCLFYEVEVNNSQTETHNVFYVQEAKCENPEFERNVENTSCFMVPGVLPDTLN 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TFILSKGRDWLAVLVNGSSKHSAIRPFDQLFALHAIDQINPPLNVTAEIEGTRLSIQWEK 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TKVKDSSFEQHSVQIMVKDNAGKIKPSFNIVPLTSRVKPDPPHIKNLSFHNDDLYVQWEN 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PPV-NFTIKVTGLAQVLLQWKPNPDQEQRNVNLEY--
                                                                                                                                                                                        ----SY----MKCSWLPGRNTSPDTNYTLYYWHRSLEKIHQCENIFRE---GQYFGCSFDL 189
                                                                                                                                                                                                                              ESKCVTILHKGFSASVRTILQNDHSLLASSWASAELHAPPGSPGTSIVNLTCTTNTTEDN 142
                                                                                                                                                                                                                                                                                                          PPV-NFTIKVTGLAQVLLQWKPNPDQEQRNVNLEY-----QVKINAPK-EDDYETRIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ----SY---MKCSWLPGRNTSPDTNYTLYYWHRSLEKIHQCENIFRE--GQYFGCSFDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ESKCVTILHKGFSASVRTILQNDHSLLASSWASAELHAPPGSPGTSVVNLTCTTNTTEDN 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ERICLQV-----GSQCSTNESEKPSILVEKCIS----PPEGDPESAVTELQCIWHNL---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ch 9.9%;
1 Similarity 24.8%;
82; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Devos, R.; Cornelis, S.; Tuypens, T.;
                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                    9.98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NID:g186387; PID:g186388 transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                  ; Score 229; DB 2;
; Pred. No. 1.2e-10;
51; Mismatches 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Score 230; DB 2;
; Pred. No. 9.6e-11;
51; Mismatches 145
  YLQIEKLMTNAFISIIDDLSKY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17-Jan-1992 #text_change 10-Sep-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -----QVKINAPK-EDDYETRIT 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      145;
                                                                                                                                                                                                                                                                                                                                                                                                                        Length 335
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                                                                                                                                                                                                                                                                                                                                                                                    Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R; (appcld,
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Best Local S
Matches 90
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256
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                309 TYRIRVKYNKLCYEDDKLWSNWSQEMSIGKKR
                                                                                                                                                                                                                                                                    90
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C:Genetics:
A:Gene: GDB:CSF2RA; CSF2R
A:Gene: GDB:CSF2RA; CSF2R
A:Cross-references: GDB:118777; OMIM:306250;
A:Map position: Xp22.32-Xp22.32; Yp11.3-Yp11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C, Keywords: glycoprotein; growth factor receptor; transmembrane protein F;1-22/Domain: signal sequence #status predicted <SIG> F;1-23/Domain: signal sequence #status predicted <SIG> F;3-32-340/Product: granulocyte-macrophage colony-stimulating factor receptor #status predicted <TMM> F;322-346/Domain: transmembrane #status predicted <TMM> F;46,54,99,123,135,182,195,223,229,272,305/Binding site: carbohydrate (Asn) (covalent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Accession: S06945; A41286; A44474
R;Gearing, D.P.; King, J.A.; Gough, N.M.; Nicola, N.A.
EMBC J. 8, 3667-3676, 1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           E;Fesidues: TM',377-400 <RAP>
P;Cross-references: GB:S48539; NID:g258858; PID:g258859; NID:g258858; PID:g258859; NID:g258858; PID:g258859; NOTE: Sequence extracted from NCBI backbone (NCBIP:11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R; Cappeld, G.; Willson, T. Genomics 14, 455-461, 1992
A;Title: Arrangement and 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;C/oss-ref:rences: EMBL:X17648; NID:g32087; PID:g32089
R:C/C:Sier; K.E; Wong, G.G.; Mathey-Prevot, B.; Nathan, D.G.; Sieff, Proc. Natl. Acad. Sci. U.S.A. 88, 7744-7748, 1991
R:Title: L. furctional isoform of the human granulocyte/macrophage co.A;Reference number: A41286; MUID:91352066
A:Accession: A41286
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               qx/annlocyte-macrophage colony-stimulating factor receptor A
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A/Status: preliminary; not compared with conceptual translation
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A:Fesidues: 347-400 <CRO>
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                                                                                                                           196 GTSREIGIQFFDSLLDTKKIERFNPPSNVTVRCNTTHCLVRWKQPRTYQKLSYLDFQYQL
                                                                                                                                                                                                                                                                                                                    150 RNTSPDTNYTLYYWHRSLEKIHQCENIFRE-GQYFGCSFD-LTKVKDSSFEQHSVQIMVK 207
                                                                 263 EVN -- NSQTETHNVFYVQEAKCENPEFERNVENTSCFMVPGVLPDTLNTVRIRVKTNKLC 320
                                                                                                                                                                                               208 DNACKIKPSF--NIVPLTSRVKPDPPHIKNLSFHNDDLYVQWENPQNF--ISRCLF-YEV 262
                                                                                                                                                                                                                                                                                                                                                                                            82 TFREICLHEGVTFEVHVNTSORGFOOKLLYPNSGREGTAAQNFSCFIYNADLMNCTWARG 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  29 TVAPASSLNVRFDSR-TMNLSWDCQENTTFSKCFL----TDKKNRVVEPRLSNNECSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
wes 90; Conserv
                                                                                                                                                                                                                                                                 PTAPRDVQYFLYIRNSKRRREIRCPYXIQDSGTHVGCHLDNLSGLTSRNY------FLVN 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                             LNER:CLQVGSQCSTNESEKPSILVEKCISPPEGDPESAVTELQCIWHNLSYMKCSWLPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TQPPVTNLSVSVENLCTVIWTWNPPEGAS-SNCSLWYFSHFGDKQDKKIAPETRRSIEVP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9.8%; Score 228; DB 2; larity 22.4%; Pred. No. 1.7e-10; Conservative 82; Mismatches 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 T.A.; Henke, A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 localization of 74; MUID:93052350
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YNFPSSEPRAKHSVKIRAADVRIL
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R:Cao, X.; Kozak, C.A.; Liu, Y.
Proc. Natl. Acad. Sci. U.S.A. 90, 8464-8468, 1993
A;Title: Characterization of cDNAs encoding the murine
A;Reference number: A47514; MUID:93391374
A;Accession: I49280
                                                                                                                                                                 C;Species: Mus musculus (house mouse)
C;Date: 27-Feb-1997 #sequence_revision 27-Feb-1997 #text_change
C;Accession: 149280; A47514; JN0592; JN0775; S37582; I53398
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A; Accession:
                               A; Molecule type: DNA
A; Residues: 1-369 < CAO>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Date: 18-Aug-1995 *sequence_revision C;Accession: A55718 R;Henthorn, P. S.; Somberg, R.L.; Fimlan Genomics 23, 69-74, 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT
A55718
                                                                                                                                                                                                                        interleukin-2 receptor gamma chain precursor -
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A; Residues: 1-373 <HEN>
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C:Species: Canis lupus familiaris (dog)
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                Cross-references:
                                                                                                                                                                                                                                                                                                                                                                                       233
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         133 --RDPREPRRQSTQKLKLQNLVIPWAP--ENLTLHNLSESQLELSWSN--RHLDHCLEHV 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   205
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                                                                                                                                                                                                                                                                                                                                                      dId
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VPLNERICLQVGSQCSTNESEKPSILVEKCISPPEGDPESAVTELQCIWHNLSYMKCSWL 147
                                                                                                                                                                                                                                                                                                                                                                                  SAOR-WSEWSHPIHWGSNTSKENPLFASEAVLIPLGSMGLIISLICVYYWLER----SIP
                                                                                                                                                                                                                                                                                                                                                                                                                   EDDKLWSNWSQEMSIGK--KRNSTLYITMLLIVPVIVAGAIIVLL---LYLKRLKIIIFP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VEVNNSQTETHNVFYVQEAKCENPEFERNVENTSCFMVPGVLPDTLNTVRIRVKTNKLCY 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MVKDNAGKIKPSFNIVPLTSRVKPDPPHIKNLSFHN----DDLYVQWENPQNFISRCLFYE 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PGRNTSPDTNYTLYYWHRSL--EKIHQCEN-IFREGQYFGCSFDLTKVKDSSFEQHSVQI 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VGLNSTVFMPNG-----NEDITPDFFLTATPSETLSVSSLPLPEVQCFVFNVEYMNCTWN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      YEDDKLMSNWSQEMSIGKKRNS--TLYITMLLIVPVIVAGAIIVLLLYLKRLKI-IIFPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                            VQYRSDWDRSWT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SSSEPRP-TNLTLHYWYKNSNDDKVQECGHYLFSREVTAGCW--LQKEEIHLYETFVVQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VPQ----IKDKLNDNHEVEDEIIWEEFTPEEGKGYREEVLTV 396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IPDPGKIFKEMFGDQN--DDTLHWKKYDIYE-KQTKEETDSV 416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Z.
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            EMBL: U21795;
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25.1%;
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           NID: 9727349; PIDN: AAA64279.1;
                                                                from GB/EMBL/DDBJ
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Pred.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            207;
No. 7
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           PID:g727350
                                                                                                               2 receptor
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                                                                                                               (IL-2R)
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A;Pathway: interleukin-2 stimulated growth and differentiation of T cell C:Superfamily: interleukin-2 receptor gamma chain C:Superfamily: interleukin-2 receptor gamma chain c:Keywords: cytokine receptor; duplication; glycoprotein; transmembrane F:1-22/Domain: signal sequence *status predicted <SIG>F:2-365/2roduct: interleukin-2 receptor gamma chain *status predicted <F:25-6-284/Domain: transmembrane *status predicted <TMM>F:71,75,84,96,159,164,306/Binding site: carbohydrate (Asn) (covalent) *s
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A:Description: receptor for interleukin-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A:Introns: 39/1; 90/2; 152/1; 199/3; 254/1; 286/2; 308/3
C:Complex: The high affinity receptor is a heterotrimer of alpha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A:Cross-references: EMBL:X75337

R:CLSanto, J.P.; Certain, S.; Wilson, A.; MacDonald, H. Exr J. Immunol. 24, 3014-3018, 1994

A:Mittle: The murine interleukin-2 receptor gamma chain A:Reference number: 153398; MUID:95104285

A:Accession: 153398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Reference number: S37582
A;Recession: S37587
A:Secession: S37587
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A/Title: Cloning and sequencing of the cDNA encoding A/Reference number; JN0775; MUID:93366191
A:Accession: JN0775
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A:Cross-references: GB:S75852; NID:g861554; PIDN:AAB32904.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: DNA
A; Residues: 1-369 < RES>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: mRNA
A; Residues: 1-350,'S',352-366,'S',368-369
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     submitted to the EMBL Data Library, October
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R; Chiu, R.K.; Dougherty,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: DDBJ:D13565; NID:g303684; PIDN:BAA02760.1; R:Kobayashi, N.; Nakagawa, S.; Minami, Y.; Taniguchi, T.; Kono.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Mclecule type: mRNA
A; Residues: 1-369 < KUM>
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A; Residues: 1-369 < RE
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Best Local :
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Residues: 1-369 < KOB>
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140
                                                                                                                                                                                                                 160 LYYWHRSLEKIHQCENIFREGQYFGCSFDLTKVKDSSFEQHSVQ-----IMVKDNAGKI
                                                                                                                                                                                                                                                                                                                          103
                                                                                                                      214 KPSFNIVPLTSRVKPDPPHIKNLSFHN---DDLYVQWENPQNFISRCLFYEVEVNNSQTE
                                                                                                                                                                             87
                                                                                                                                                                                                                                                                             ^{\omega}_{\perp}
                                                                                                                                                                                                                                                                SANEDIKADLILTSTAPEHLSAPTLPLPEVQCFVFNIEYMNCTW----NSSSEPQATNLT
                                                              RRAVQKLNLQNLVIPRAP--ENUTLSNLSESQLELRWKS-RHIKERCLQYLVQYRSNRDR 196
                                                                                                                                                                                                                                                                                                                STNESEKPSILVEKCISPPEGDPESAVTELQCIWHNLSYMKCSWLPGRNTSPD---TNYT 159
                                                                                                                                                                   LHYRYKVSD-----NNTFQECSHYLFSKEIT--SGCQIQKEDIQLYQTFVVQLQDPQKPQ 139
                                                                                                                                                                                                                                                                                                                                                                        76; Conser
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larity 24.0%;
Conservative 6
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                                                                                                                                                                                                                                                                                                                                                                        63;
                                                                                                                                                                                                                                                                                                                                                                   Score 205.5; DB 2;
Pred. No. 9.1e-09;
3; Mismatches 121;
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                                                                                                                                                                                                                                                                                                                                                                     57;
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A;Gene: GDB:IL2RG; SCIDX1; IMD4
A;Cross-references: GDB:i34807; OMIM:308380
A;Map position: xq13.1-xq13.1
A;Introns: 39/1; 90/2; 152/1; 198/3; 253/1; 285/2; 308/3
A;Note: defects are associated with an X-linked form of severe combined.
C;Superfamily: interleukin-2 receptor gamma chain
C;Keywords: cytokine receptor; duplication: immunodeficience.
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A;Title: Characterization of the human interleukin-2 A;Reference number: A46591; MUID:93293887
A;Accession: A46591
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R:Takeshita, T.; Asao, H.; Ohtani, K.; Ishii, N.; Kumaki, S.; Science 257, 379-382, 1992
A;Title: Cloning of the gamma chain of the human IL-2 receptor A;Reference number: A42565; MUID:92335883
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Best Local Similarity 27.2
Matches 72; Conservative
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:Residues: 1-369 <R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  um. Mol. Genet. 2, 1099-1104, 1995
Title: The interleukin-2 receptor gamma chain maps to Reference number: I54332; MUID:94004847
Accession: I54332..... translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Status: preliminary; translated
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Molecule type: nucleic acid; Residues: 1-369 <TAK>
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Accession: A42565; A46591; I54332
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     301
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GVLPDTLNTVRIRVKTNKLCYEDDKLWSNWSQEMSIG---KKRNSTLYITMLLIVPVIVA 357
                                                                                                       VQWENPQNFISRCL----FYEVEVNNSQTETHNVFYVQEAKCENPEFERNVENTSCFMVP 300
                                                                                                                                                                                                               DLTKVKDSSFEQHSVQIMVKDNAGKIKPSFNIVPLTSRVKPDPPHIKNLSFH---NDDLY 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        preliminary; translated from GB/EMBL/DDBJ
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                                                     LNWNN--RFLNHCLEHLVQYRTDWDHSWT--
                                                                                                                                                          QLQKKEIHLYQTFVVQL--QDPREPRRQATQMLKLQNLVIPWAP--ENLTLHKLSESQLE 171
                                                                                                                                                                                                                                                                  EVQCFVFNVEYMNCTWNSSSEPQP-TNLTLHYWYKNSDNDKVQKCSHYLFSEEITSGC-- 116
                                                                                                                                                                                                                                                                                                                    ELQCIWHNLSYMKCSWLPGRNTSPDTNYTLYYWHRSL--EKIHQCEN-IFREGQYFGCSF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KWSQPVHWGSHTVEENPSLFALEAVLIPVGTMGLIITLIFVYCWLERM-----PPIP-PI 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NWSQEMSIGK---KRNSTLYITMLLIVPVIVAGAIIVLLL---YLKRLKIIIFPPIPDPG 382
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1-369 <RE2>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GB:L19546; NID:g349631; PIDN:AAC37524.1; PID:g349632
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                                                                                                                                                                                                                                                                                                                                                                                                   8.78;
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                                                                                                                                                                                                                                                                                                                                                                             44;
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Pred. No. 1.7e-08;
4; Mismatches 101
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C: Yeywords: glycoprotein; transmembrane protein
F:1-23/Domain: signal sequence #status predicted <SIG>F:24-831/Product: prolactin receptor #status predicted <MAT>
E:439-462/Domain: transmembrane #status predicted <TMM>F:54,39-462/Domain: transmembrane #status predicted <TMM>F:54,91,100,112,132,262,303,315,335,647,701,800/Binding site:
                                                                                                          C:Date: 13-Jul-1990 #sequence_revision 09-Oct-1992 #text_change 10-Sep-1997
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Siochem. Biophys. Res. Commun. 188, 490-496, 1992
A;Title; Double antenna structure of chicken prolactin
A;Reference number: JQ1655; MUID:93075121
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                                               R;Zhang, R.; Buczko, E.; Tsai-Morris, C.H.; Hu, Z.Z.;
Biochem. Biophys. Res. Commun. 168, 415-422, 1990
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A; Residues: 1-83] <TAN>
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                                                                                           C; Accession:
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                                                                                                                                                                                                                  RESULT 11
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C; Species: Gallus yallus (chicken)
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                                                                                                                                                                   lactogen receptor i.-
Northem. Biophys. Res. Commun. 168, 415-422, 1990 rittle: Isolation and characterization of two novel Reference number: A34631; MUID:90241201
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                                                                                                                                                                                                                                                                                     445 LGVLSSLICLIMSWTMVLKGYRMITFMLPPVPGP
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                                                                                                                                                                                                                                                                                                                                     353 PVIVAGATIVLL---LYLKRIKTIF--PPIPDP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             344 INRKPYLVLTWSPPPLADVRSGWLTLEYELRLKPEEGEEWETIFVGQ-QTQYKMFSLN--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     183 YEGCSEDLTKVKDSSFEQHSVQIMVKDNAGKIKPSENIVPLTSRVKPDPP-----HIKNL 236
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  212 SVEGOKRYTERVRSRENPLC-GSAQHWSEWSHPIHWGSNTSKENPFLFALEAVVISVGSM
                                                                                                                                                                                                                                                                                                                                                                                                                              293 NTSCFMVPGVLPDTLNTVRIRVKTNKLCYEDDKLWSNWSQEMSIGKKRNSTLYITMLLIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         286 PNSCYFD--KKHTSFWTIYNTTVRATNEMGSNSSDPHYVDVTYIVQPDPPVNVTLELKKP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    85 SIEVPLNERICLQVGSQCSTNE---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              32 QP - PYTHLSYSYENICTY - IWT-WNPP - - EGASSNCSLWYFSHFGDKQDKKIAPETRR 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30-Sep-1993 #sequence_revision 30-Sep-1993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       F-----KPTIIKCRSPEKETFTCWWKPGLDGGHPTNYTLLYSKEGEEQVYECPD-YRTAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EWET---:-ISVGVQTQCKINRLNAGMRYVVQVRCTLDPGEWSEWSSERHILIPSGQSPP
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23.1%;
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A; Residues: 1-610 <SHI>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MO1. Endocrinol. 4, 1136-1143, 1990
A:Title: Expression of two forms of prolactin
A;Reference number: A36116; MUID:91155946
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              prolactin receptor 2 precursor - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 28-Mar-1991 #sequence_revision 28-Mar-1991 #text_change 10-Sep-1997
C;Accession: A36116
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A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-610 <ZHA>
A;Cross-references: GB:M34083; NID:g205122; PID:g205123
A;Note: the authors translated the codon GAG for residue
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                                 RNSTLYITMLLIVPVIVAGAIIVLLLYLKRLK-----IIIFPPIPDP
                                                                                              AKCENPEFERNVENTSCFMVPGVLPDTLNTVRIRVKTNKLCYEDDKLWSNWSQEMSIGKK 339
                                                                                                                                                                                                                                KIHQCENIFREGQYFGCSFDLTKVKDSSFEQHSVQIMVKDNAGKIKPSFNIVPLTSRVKP 228
                                                                                                                                EPPRNLTLEVKQLKDKKTYLWVKWSPPTITDVKTGWFTMEYEIRLKPEEAEEWEIHF---
                                                                                                                                                             DPP----HIKNLSFHNDDLYVQWENPQNFISR----CLFYEVEVNNSQTETHNVFYVQE 279
                                                                                                                                                                                               TTYECPDYKTSGPN-SCFF--SKQYTSTWKIYIITVNATNQMGSSSSDPLYVDVTYIVEP
                                                                                                                                                                                                                                                                KPEI--HKCRSP---DKET------FTCWWNPGTDGGLPTNYSLTYSKEGEK 65
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23.7%;
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23.7%; Pred. No. 3.4e-07;
tive 43; Mismatches 120;
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C:Keywords: transmembrane protein F:1-19/Domain: signal sequence #status predicted <SIG>
                                         A;Cross-references: GB:M19304; NID:g206364; PID:g206365
                                                                       A; Mclecule type: mRNA
A; Residues: 1-310 <BOU>
                                                                                                            A; Title: Cloning and expression of the rat A; Teference number: A29884; MUID:88165059 A; Accession: A29884
                                                                                                                                                                              R; Boutin, J.M.; Jolicoeur, C.; Okamura, H.; Gagnon, J.; Cell 53, 69-77, 1988
                                                                                                                                                                                                                   prolactin receptor precursor - rat
C;Species: Rattus norregicus (Norway rat)
C;Date: 30-Sep-1989 #sequence_revision 30
C;Iccession: A29884
                                                                                                                                                                                                                                                                                                          RESULT
A29884
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A;Accession: I55417
A,Status: translated from GB/EMBL/DDBJ
A;Mclecule type. .....
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R.O'Neal, K.D.; Yu-Lee, L.Y.
J. Biol. Chem. 269, 26076-26082, 1994
A. Title: Differential signal transduc
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J. Biol. Chem. 266, 20110-20117, 1991
A:Title: A prolactin-dependent immune cell
A:Reference number: A41070; MUID:92041834
A:3-cession: A41070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Mclecule type: mRNA
A; Residues: 1-412 < RES>
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C:Sproies: Rattus norvegicus (Norway rat)
C:Date: 12-Jun-1992 #sequence_revision 12-Jun-1992 #text_change 10-Sep-1997
C:Accession: A41070; I55417
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A; Fosidues: 1-412 <ALI>
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Best Local Similarity 23.7%;
Matches 68; Conservative 4
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Pred. No. 2.1e-07;
3; Mismatches 120
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F; 20-310/Product:

prolactin receptor #status predicted

**AMAT** 

Length 310;

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Best Local Similarity
Matches 80; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Species: Bos primigenius taurus (cattle)
Date: 16-Aug-1996 #sequence_revision 16-Aug-1996 #text_change 28-Feb-1997
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                                               386 KEMFGDQNDDTLHWKKYDIY -- EKQTKEE 412
                                                                                                                                                                                                    182 THFTLKQTQLKIFN---------LYPGQKYLVQIR-----CKPDHGYWSEW
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                                                                                                                                                                                                                                                                                                                                                                                                         70 TLIHECPD-YKTGGPNSCYF--SKKHTSIWKMYVITVNAINQMGISSSDPLYVHVTYIVE 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               66 TIYECPDYKTSGPN-SCFF--SKQYTSIWKIYIITVNATNQMGSSSSDPLYVDVTYIVEP 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25
                                                                                                                                                  SQEMSIGKKRNSTLYITMLLIVPVIVAGAIIVLLLYLKRLK-----IIIFPPIPDPGKIF 385
                                                                                                                                                                                                                                                                                                      PEPP--ANLTLELKHPEDRKPYLWIKWSPPTMTDVKSGWFI---IQYEIRLKPEKATDWE 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EKPKLV -- KCRSPGK ---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    preliminary; translated from GB/EMBL/DDBJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              er, M.A.; Schuler, L.A. nol. 89, 47-58, 1992
-KGFDVHLLEKGKSEE 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            of the bovine prolactin receptor and distribution of prolact MUID:93246019
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  44; Mismatches 115;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 186; DB 2;
Pred. No. 5.6e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -----ETFTCWWEPGADGGLPTNYTLTYHKEGE 69
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January 19, 2000, 14:58:50

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# GenCore version 4.5 Copyright (c) 1993 - 1998 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 20, 2000, 06:19:55; Search time 35.05 Seconds (without alignments) 354.343 Million cell updates/sec

Title: Perfect score: Sequence:

US-09-077-817-4
2324
1 MEMPARICGLWALLICAGGG......QTKEETDSVVLIENLKKASQ 427

Searched: Scoring table: BLOSUM62 80000 seqs, 29085965 residues

Database : SwissProt\_38:\*

Word size :

Number of hits that pass the threshold : 80000

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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٠.	IL4R_HUMAN	EPOR_MOUSE	EPOR_RAT	INR1_BOVIN	GHRH_MOUSE	INR1_HUMAN
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## ALIGNMENTS .

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	EMBL; Y10659; CAA71669.1;	nd an email to license@isb-sib.ch).	license agreement (See http://www.is	as its content is	rmatics Institute. There are no restrictions on	een the Swiss Institute of Bioinfo	s SWISS-PROT entry is copyright. It is produced through	IMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.		-!- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.	KIDNEY. ALSO FOUND IN B-CELLS, T-CELLS AND ENDOTHELIAL CELLS.	SKELETAL MUSCLE AND OVARY: LOWEST LEVELS IN BRAIN, LUNG A			-!- SUBUNIT: INTERLEUKIN-13 RECEPTOR IS A COMPLEX OF IL4R-ALPHA,	ALLOWING ENHANCED IL-2 BINDING ACTIVITY.	CHAIN FOR IL-4 SIGNALING, BUT CANNOT REPLACE THE PUNCTION OF	ALPHA CAN FORM A FUNCTIONAL RECEPTOR FOR IL-13. ALSO SERVES	TION: BINDS IL-13 WITH A LOW AFFINITY. TOGETHER WITH IL-4R-	Sicl. Chem.	"CDNA CIONING AND CHAFACLERIZACION OF THE NUMBER INCERTEURIN IS		N., OBIR	184. 0	TISSUE-T-CELL	SECTION OF FROM N. A.	Submitted (Jan-1997) to the EMBL/GenBank/DDBJ databases.		., WELLS T.	E FENC N D MOCED	SEQUENCE FROM N.A.		. 401:163-166(1997).	ILAR alpha of a functional IL-4/IL-13 receptor complex.":	+ho hims II -100 alabal obsis and soccessive the	MILOUX B., LAURENT P., BONNIN O., LUPKER J., CAPUT D., VITA N.,	HEDLINE: 97165986	SEQUENCE FROM N.A.		Catarrhini; Hominidae; Homo.	Bomo Sapiens (numan). - Enkaryotas Matazoa: Chordata: Craniata: Vertebrata: Mammalia:	ILI3RAI OR ILI3RA OR ILI3R.		INTERLEUKIN-13 RECEPTOR ALPHA-1 CHAIN PRECURSOR (IL-13R-ALPHA-1) (IL-	01-NOV-1997 (Rel. 35, Last sequence update)	(Rel.	I131_HUMAN STANDARD; PRT; 427 AA.	I 3 1 HUMAN	

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ID 1131_MOUSE

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Last sequence update
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                                                                                                                                                                                                                                                                                                                                                                         Score 2324; DB 1; Length Pred. No. 1.3e-171; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                   POTENTIAL
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N REF. 3).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13 receptor that is also a component of the interleukin 4 recept Proc. Natl. Acad. Sci. U.S.A. 93:497-501(1996).
1: FUNCTION: BINDS IL-13 WITH A LOW AFFINITY. TOGETHER WITH IL-ALPHA, CAN FORM A FUNCTIONAL RECEPTOR FOR IL-13. ALSO SERVES ALTERNATE ACCESSORY PROTEIN TO THE COMMON CYTOKINE RECEPTOR CHAIN FOR IL-4 SIGNALING, BUT CANNOT REPLACE THE FUNCTION OF
                                                                                                                                                                                                                                                                                                  CARBOHYD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. MEDLINE; 96133964.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15-JUL-1999 (Rel. 38, Last annotation update)
INTERLEUKIN-13 RECEPTOR ALPHA-1 CHAIN PRECURSOR (IL-13R-ALPHA-1)
13RA-1) (INTERLEUKIN-13 BINDING PROTEIN) (NR4).
IL13RA1 OR IL13RA OR IL13R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MGD; MGI:105052;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HILTON D.J., ZHANG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Cloning and characterization of a binding subunit of the
                                            59
                                                                                                                                                                      Local Similarity
nes 319; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SIMILARITY).

SIBUINT: INTERLEUKIN-13 RECEPTOR IS A COMPLEX OF IL4R-ALPHISTBUDINT: INTERLEUKIN-13 RECEPTOR IS A COMPLEX OF IL4R-ALPHILIBR-ALPHA, AND POSSIBLY OTHER COMPONENTS (BY SIMILARITY)

SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

TISSUE SPECIFICITY: SPLEEN, LIVER, THYMUS, HEART, LUNG, KII
TESTIS, STOMACH, BRAIN, SKIN, AND COLON; BUT NOT SKELETAL I
SIMILARITY: CONTAINS 1 IMMUNOCLOBULIN-LIKE C2-TYPE DOMAIN.
SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
                                                                                                                        MEWPARLCGLWALLLCAGGGGGGGAAPTETQPPVTNLSVSVENLCTVIWTWNPPEGASS
                                          NCTLRYFSHFDDQQDKKIAPETHRKEELPLDEKICLQVGSQCSANESEKPSPLVKKCISP
                                                            NCSLWYFSHFGDKQDKKIAPETRRSIEVPLNERICLQVGSQCSTNESEKPSILVEKCISP
                                                                                                        MARPALIGELLVILLWT--ATVGQVAAATEVQPPVTNLSVSVENLCTIIWTWSPPEGASP
PEGDPESAVTELQCIWHNLSYMKCSWLPGRNTSPDTNYTLYYWHRSLEKIHQCENIFREG
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IL-13 WITH A LOW AFFINITY. TOGETHER WITH IL-4R-
THE TOGETHER WITH IL-4R-
THE TOGETHER WITH IL-4R-
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                                                                                                                                                                                                                                                  48402 MW;
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Pred. No. 1.6e
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ol-MAY-1991 (Rel. 18, Created)
Ol-MAY-1991 (Rel. 18, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
INTERLEUKIN-5 RECEPTOR ALPHA CHAIN PRECURSON
ILSRA OR ILSR.
Mus musc.
  DOMAIN
DISULFID
DISULFID
                                                                                                                                                         use by non-profit institute. There are no restrictions modified and this statement is not removed. Usage by and for comentities requires a license agreement (See http://www.isb-sib.ch/anuor send an email to license@isb-sib.ch).
                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus (Mouse).

Motazoa; Chordata;
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                                       TRANSMEM
                                                               CHAIN
                                                                           SIGNAL
                                                                                                                                                EMBL;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
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                                                   DOMAIN
                                                                                                   PROSITE;
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                                                                                                                                                                                                                                                                                                          SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA CHAIN. THE BETA CHAIN IS COMMON TO THE IL-3, IL-5 AND GM-CCSF RECEPTORS. SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
TISSUE SPECIFICITY: EXPRESSED ON EOSINOPHILS AND BASOPHILS.
                                                                                                                                                                                                                                                                          SIMILARITY:
                                                                                                                                                                                                                                                                                                                                                            FUNCTION: THIS
BINDS TO IL-5
                                                                                                                                                                                                                                                                                      SIMILARITY:
                                                                                                                                                                                                                                                                                                  ON B-CELLS.
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                                                                                  PS00241; RECEPTOR_CYTOKINES_1; FALSE_NEG PS00340; RECEPTOR_CYTOKINES_2; 1.
; Transmembrane; Glycoprotein; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rodentia;
                                                                           Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                           cloning and expression of the murine interleukin
                                                                                                                                                                                                                                                                                                                                                                                                                                   TOMINAGA A.,
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131
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                                                                                                                                                BAA14231.1; -.
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                                                                                                                                                                                                                                                                      BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS TO IL-13 RECEPTOR ALPHA-2 CHAIN.
                                                                                                                          IL5RA
   415
339
361
415
152
193
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                                                                                                                                                                                                                                                                                                                                                                                                                                    MITA
INTERLEUKIN-5 RECEPTOR ALPHA CHAIN. EXTRACELLULAR (POTENTIAL). POTENTIAL). CYTOPLASMIC (POTENTIAL). BY SIMILARITY.
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Mus.
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SEQUENCE
                                                                     SEQUENCE;
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Eukaryota; Metazoa: (
Eutheria; Primates;
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31-NOV-1997 (Rel.
ENTERLEUKIN-5 RECE
                                                                                                                                                                                                                                                   MEDLINE;
                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. MEDLINE; $2372031.
                                              TAVERNIER J.,
                                                                                                                            "Molecular basis of the membrane-anchored and two
the human interleukin 5 receptor alpha subunit.";
Proc. Natl. Acad. Sci. U.S.A. 89:7041-7045(1992).
                                                                                                                                                                                                       DEVOS R.;
                                                                                                                                                                                                                       TAVERNIER J., TUYPENS T.,
                                                                                                                                                                                                                                              SEQUENCE FROM N.A. MEDLINE; 92357767.
                                                                                                                                                                                                                                                                                                            SCOTT H.S., GUO X.H., HOPWOOD

*Structure and sequence of the
Genomics 13:1311-1313(1992).
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415 AA;
R.J., DEVOS R.,
, PLAETINCK S.;
high affinity (
                                                                   OF 1-335 FROM 92005669.
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EPTOR ALPHA CHAIN PRECURSOR
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Catarrhini; Hominidae;
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                                                                                       N.A. (S1 FORM).
    interleukin-5
                                           CORNELIS S., TUYPENS T., VAN
                                                                                                                                                                                                                         PLAETINCK G., VERHEE
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Pred. No. 2.4e-17;
4; Mismatches 179;
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n alpha-L-iduronidase gene.";
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -:- TISSUE SPECIFICITY: EXPRESSED ON EOSINOPHILS AND BASOPHILS
-:- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
-:- SIMILARITY: TO IL-13 RECEPTOR ALPHA-2 CHAIN.
-:- DATABASE: NAME-PROW; NOTE-CD guide CDw125 entry:
WWW-"http://www.ncbi.nlm.nih.gov/prow/cd/cdw125.htm".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -i- FUNCTION: THIS IS THE RECEPTOR FOR INTERLEUKIN-5. THE IBINDS TO IL-5.
-i- SUBBURIT: HETERODIMER OF AN ALPHA AND A BETA CHAIN. THE CHAIN IS COMMON TO THE IL-3, IL-5 AND GM-CSF RECEPTORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   an IL5-specific alpha chain for GM-CSF."; Cell 66:1175-1184(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PS00241; RECEPTOR_CYTOKINES_1; FALSE_NEG.
PROSITE; PS00340; RECEPTOR_CYTOKINES_2; 1.
Receptor; Transmembrane; Glycoprotein; Alternative splicing; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                the European Bioinformatics Institute.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DOMAIN
                                                            190
                                                                                                                      140
250 PQN-FISRCLFYEVEVNNSQTETHNVFYVQEAKCENPEFERNVENTSCFMVPGVLPDTLN 308
                               201
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                                                                                                                                                   83
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN. ALTERNATIVE PRODUCTS: THREE ISOFORMS, TWO SOLU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEMBRANE-BOUND FORM EXIST DUE TO ALTERNATIVE SPLICING
                                                                                                                                                                                                                                       PPVTNLSVSVENLCTVIWTWNP-PEGASSNCSLWYFSHFGDKQDKKIAPETRRSIEVPLN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       147851;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A40267; A40267.
                             TFILSKGRDWLSVLVNGSSKHSAIRPFDQLFALHAIDQINPPLNVTAEIEGTRLSIQWEK
                                                         TKVKDSSFEQHSVQIMVKDNAGKIKPSFNIVPLTSRVKPDPPHIKNLSFHNDDLYVQWEN
                                                                                       YSRLRSYQVSLHCTWLVGTDAPEDTQYFLYYRYGSWTE--ECQEYSKDTLGRNIACWFPR
                                                                                                        ----SY---MKCSWLPGRNTSPDTNYTLYYWHRSLEKIHQCENIFRE--GQYFGCSFDL
                                                                                                                                                                               ERICLQV-----GSQCSTNESEKPSILVEKCIS----PPEGDPESAVTELQCIWHNL--- 140
                                                                                                                                                                                                           PPV-NFTIKVTGLAQVLLQWKPNPDQEQRNVNLEY-----QVKINAPK-EDDYETRIT 82
                                                                                                                                                   ESKCVTILHKGFSASVRTILQNDHSLLASSWASAELHAPPGSPGTSIVNLTCTTNTTEDN
                                                                                                                                                                                                                                                                        102;
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                                                                                                                                                                                                                                                                        Conservative
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342
362
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                                                                                                                                                                                                                                                                                   12.8%;
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                                                                                                                                                                                                                                                                                   Score 296.5; DB 1;
Pred. No. 1.1e-15;
                                                                                                                                                                                                                                                                                                                                            NDE -> FSR (IN SOLUBLE ISOFORM S1).
MISSING (IN SOLUBLE ISOFORM S1).
N -> K (IN SOLUBLE ISOFORM S2).
MISSING (IN SOLUBLE ISOFORM S2).
; 75C19847 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                      POTENTIAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EXTRACELLULAR (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                        POTENTIAL.
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                                                                                                                                                                                                                                                                        Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                There are no
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  as its content
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RECEPTOR ALPHA CHAIN
                                                                                                                                                                                                                                                                      180;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOLUBLE FORMS AND
                                                                                                                                                                                                                                                                                                  Length 420;
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                                                                                                                                                                                                                                                                      16;
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Receptor; SIGNAL

PROSITE;

PS00340;

RECEPTOR\_CYTOKINES\_2; 1.

Glycoprotein; Signal

POTENTIAL.

Transmembrane;

DOMAIN

DOMAIN CHAIN

TRANSMEM

380 380 380 380

POTENTIAL.
CYTOPLASMIC (POTENTIAL).
BY SIMILARITY.

INTERLEUKIN-13 RECEPTOR ALPHA-2 EXTRACELLULAR (POTENTIAL).

CHAIN

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RESULT 5
                               EMBL; U70981;
EMBL; Y08768;
MIM; 300130;
                                                                                                                                                  use by non-profit institutions as long modified and this statement is not removed. entitles requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                     GUO J. MINVIELLE S.;
Submitted (MAR-1997) to the EMBL/GenBank/DDBJ databases
i- FUNCTION: BINDS AS A MONOMER WITH HIGH AFFINITY TO
(IL-13), BUT NOT TO IL-4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
INTERLEUKIN-13 RECEPTOR ALPHA-2 CHAIN PRECURSOR (INTERLEUKIN-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DONALDSON D.D., WHITTERS M.J., FITZ L., NEBEN T., FINNERTY H., HENDERSON S.L., O'HARA R.M. JR., TURNER K.J., WOOD C.R., COLLINS Submitted (OCT-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE=RENAL CELL CARCINOMA; MEDLINE, 96279273.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BINDING PROTEIN). IL13RA2 CR IL13R.
                                                                                                       EMBL; X95302;
                                                                                                                                                                                                                                           the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                    -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
-!- SIMILARITY: CONTAINS 1 FIBRONECTIN TYPE III-LIKE DOMAIN.
-!- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE-TESTIS;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FERRARA P.
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              PF00041;
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11; fn3; 1.
                                                            CAA70021.1;
                                                                               AAB17,170.1;
                                                                                                       CAA64617.1; -.
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IL-5 receptor alpha
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RESULT 6
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                                                                                                                                                                                                  MEDLINE; 90059900.

MEDLINE; 90059900.

GEARING D.P., KING J.A., GOUGA.

"Expression cloning of a receptor for colony-stimulating factor.";

colony-stimulating factor.";

colony-stimulating factor.";

colony-stimulating factor.";

colony-stimulating factor.";
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GMCR_HUMAN STANDARD; PRT; 400 AA. P15509; Q14429; Q14430; Q1-APR-1990 (Rel. 14, Cast sequence update) 15-JUL-1999 (Rel. 38, Last annotation update) GRANULOCYTE-MACROPHAGE COLONY-STIMULATING FACTOR CHAIN PRECURSOR (GM-CSF-R-ALPHA) (CDW116) (CD116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DISULFID
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SEQUENCE
                                        "Cloning and sequencing of the cDNAs encoding t
splicing-derived variants of the alpha subunit
granulocyte-macrophage colony-stimulating facts
Biochim. Biophys. Acta 1223:306-308(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; C
SEQUENCE OF
                                                                                                                                                       MEDLINE;
                                                                                                                                                                               TISSUE-BLOOD;
                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                 Eutheria;
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or human
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                                                               factor receptor. ";
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MAKAGAWA W., KOSTGI H., MIYAJIMA A., ARAI K.I., YOKOTA T.;

"Structure: The gene encoding the alpha subunit of the h
granulogete, macrophage colony stimulating factor receptor.

Implications for the evolution of the cytokine receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         use by non-profit institutions as long modified and this statement is not removed entities requires a license agreement (See or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -i- ALTERNATIVE PRODUCTS: AT LEAST 3 ISOFORMS, GM-CSF-R-ALP
HERE) TO GM-CSF-R-ALPHA-3, ARE PRODUCED BY ALTERNATIVE
-i- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS
                                                                                                                                                                              CARBOHYD
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                                                                                                                                                                                                                                                                                                                                                                                                              EMBL;
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IS PROBABLY SOLUBLE.
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 SEQUENCE
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                                                                                                                                                                                                                                                                                                                                     PSJJ241; RECEPTOR_CYTOKINES_1; 1. PSJ0340; RECEPTOR_CYTOKINES_2; 1. Transmembrane; Glycoprotein; Sig
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                                                        POTENTIAL.

INTERPRETARIAN -> VVLTTGTSALCTFMCS (IN GN-CSF-R-ALPHA-2),

MISSING (IN GM-CSF-R-ALPHA-2).

GSDDGNLGSVYIYVLLIVGTLVCGIVLGFLFKRFLRIQRLF
                                                                                                                    POTENTIAL.
                                                                                                                                                     POTENTIAL.
                                                                                                                                                                                         POTENTIAL.
                                 PPVPQIKDKLNDNHEVEDEIIWEEFTPEEGKGYREEVLTVK
EIT -> DDHLGGIHPRGRERLPRRGLDREGNYLRPRGCRN
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BY SIMILARITY
                                                                                                                                                                                                                                                                                       FACTOR RECEPTO
           R-ALPHA-3
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                       GMDISASATRGNCFLDDAVNLYIIFYVFI
                                                                                                                                           FOTENTIAL.
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ELLULAR (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                      Signal; Alternative
  CRC32
                                                                                                                                                                                                                                                                 (POTENTIAL)
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MBL outstation -
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Best Local
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                                                                                         INTERLEUKINS.

-!- SUBBUNIT: THE GAMMA CHAIN IS COMMON TO THE IL-2, IL-4, IL-7 AN PROBABLY ALSO THE IL-13 RECEPTORS.
-!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN:
-!- DISEASE: DEFECTS IN IL2RG ARE THE CAUSE OF A CANINE X-LINKED SEVERE COMBINED IMMUNODEFICIENCY.
-!- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
-!- SIMILARITY: CONTAINS 1 FIBRONECTIN TYPE III-LIKE DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-EB-1995 (Rel. 31, Created)
01-EEB-1995 (Rel. 31, Last sequence update)
01-EEB-1995 (Rel. 31, Last sequence update)
15-UL-1998 (Rel. 36, Last annotation update)
CYTOKINE RECEPTOR COMMON GAMMA CHAIN PRECURSOR (GAMMA-C)
CYTOKINE RECEPTOR GAMMA CHAIN) (IL-2R GAMMA CHAIN) (P64).
                                                                                                                                                                                                                                                       Genomics 23:69-74(1994)
                                                                                                                                                                                                                                                                                severe combined immunodeficiency
                                                                                                                                                                                                                                                                                                                             HENTHORN P.S., SOMBERG R.L., FIMIANI V.M.,
                                                                                                                                                                                                                                                                                                                                                                                                            Canis familiaris (Dog).
Canis familiaris (Dog).
Therworks: Metagoa; Chordata; Craniata; Vertebrata;
                                                                                                                                                                                                                                                                             "IL-2R gamma gene microdeletion demonstrates that severe combined immunodeficiency is a homologue of
                                                                                                                                                                                                                                                                                                                      FELSBURG P.J.
                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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                                                                                                                                                                                                                           FUNCTION: COMMON SUBUNIT FOR THE RECEPTORS FOR A VARIETY OF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IPDPGKIFKEMFGDQN--DDTLHWKKYDIYE-KQTKEETDSV 416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 YEDDKLWSNWSQEMSIGKKRNS--TLYITMLLIVPVIVAGAIIVLLLYLKRLKI-IIFPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-----WSSWSEAIEFGSDDGNLGSVYIYVLLIVGTLVCG-IVLGFLFKRFLRIQRLFPP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNAGKIKPSF--NIVPLTSRVKPDDPHIKNLSFHNDDLYVQWENPQNF--ISRCLF-YEV 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PTAPRDVQYFLYIRNSKRRREIRCPYYIQDSGTHVGCHLDNLSGLTSRNY-----FLVN
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90; Conserv
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ilarity 22.4%;
Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
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Pred. No. 1.
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.9e-10;
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RESULT 8
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Best Local
                                                                           01-FEB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
01-FEB-1998 (Rel. 37, Last annotation updat
CYTOKINE RECEPTOR COMMON GAMMA CHAIN PRECUP
                                                                                                                                     CYRG_MOUSE
P34902;
01-FEB-1994
                                                    Eukaryota;
      SEQUENCE FROM N.A. MEDLINE; 93277575.
                                                               Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CARBOHYD
CARBOHYD
SEQUENCE
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CARBOHYD
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                                                                                                                                                                                                                                                                                322 EDDKLMSNWSQEMSIGK--KRNSTLYITMLLIVPVIVAGAIIVLL---LYLKRLKIIIFP
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                                                                                                                                                                                                                                                                                                                                                                                                                           148 PGRNTSPDTNYTLYYWHRSL--EKIHQCEN-IFREGQYFGCSFDLTKVKDSSFEQHSVQI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PFAM; PF00041;
                                                                                                                                                                                                                                                                                                                                                                                                     76 SSSEPRP-TNLTLHYWYKNSNDDKVQECGHYLFSREVTAGCW--LQKEEIHLYETFVVQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                            21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        88 VPLNERICLQVGSQCSTNESEKPSILVEKCISPPEGDPESAVTELQCIWHNLSYMKCSWL 147
                                                                                                                                                                                                                       RIP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   VGLNSTVPMPNG-----NEDITPDEFLTATPSETLSVSSLPLPEVQCFVFNVEYNNCTWN 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        76;
                                                                                                                                                                                                                      290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                         Rodentia;
                                                   Metazoa;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Transmembrane; Glycoprotein; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                            STANDARD;
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                                    Chordata; Craniata; Vertebrata;
Sciurognathi; Muridae; Murinae;
                                                   Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RECEPTOR_CYTOKINES_1; 1.
RECEPTOR_CYTOKINES_2; FALSE_NEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8.9%;
25.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               42516 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 207; DB 1;
Pred. No. 7.3e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           POTENTIAL.
POTENTIAL.
                                                                                                                                                           PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CYTOKINE RECEPTOR COMMON GAMMA CHAIN. EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                         -EQSVDHRNSFSLPSVDGQKFYTFRVRSRYNPLCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches 131;
                                                                                  on update)
N PRECURSOR (GA
) (IL-2R GAMMA
                                                                                                                                                         369
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                                                                                                                                                         A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (POTENTIAL).
                                                                                 . (GAMMA-C)
MMA CHAIN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 373;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                 (P64).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   44;
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KONDO M.,

TAKESHITA T.,

ASAO

Ή.,

NAKAMURA M.,

SUGAMURA K.;

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EMBL;
EMBL;
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EMBL;
EMBL;
PIR;
                                                                                                                                             EMBL;
EMBL;
                                                                                                                                                                                        EMBL;
EMBL;
                                                                                                                                                                                                                                                       the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                   INTERLEUKINS.

1. SUBUNIT: THE GAMMA CHAIN IS COMMON TO THE IL-1
PROBABLY ALSO THE IL-13 RECEPTORS.

1. SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

1. SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF
                                                                                                                                                                              EMBL;
                                                                                                                                                                                                                                   entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the El
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "The murine interleukin-2 receptor gamma chromosomal localization and expression i Eur. J. Immunol. 24:3014-3018(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CAO X., KOZAK C.A., LIU Y.J., NOGUCHI M., O'CONNELL E., LEONARD "Characterization of cDNAs encoding the murine interleukin 2 rec [IL-2R] gamma chain: chromosomal mapping and tissue specificity
                                                                                                                                                                                                                                                                                                                                                                                          J. Neurooncol. 26:231-239(19)
                                                                                                                                                                                                                                                                                                                                                                                                                                        CHIU R.K., DRO DOUGHERTY G.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
MEDLINE; 93366191.
KOBAYASHI N., NAKAGAWA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Cloning of the mouse interleukin 2 recedemonstration of functional differences receptors.";
                                                                                                                                                                                                                                                                                                                                                                                                               the adhesion protein CD44
                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE; 96341745.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3ene 130:303-304(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IL-2R gamma chain expression.
Proc. Natl. Acad. Sci. U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-CBA/CA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Biochem. Biophys. Res.
                                                                                                                                                                                                                                                                                                                                                                                                                      'Molecular mechanisms regulating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cloning and sequencing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SANTO J.P., CERTAIN S., WI
                                                                                                                                                                                                                                                                                                                         SIMILARITY: CONTAINS 1 FIBRONECTIN TYPE III-LIKE DOMAIN.
                                                   ; x75337; CAA53085.
JN0592; JN0592.
JN0775; JN0775.
                               MGI:96551; IL2RG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        J. Immunol.
                                                                                                                                                                                                   D13821;
U21795;
                     PF00041; fn3;
                                                                                                                                                                              L20048;
                                                                                                                                                                                         D13565;
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PS00241; RECEPTOR_CYTOKINES_1; PS00340; RECEPTOR_CYTOKINES_2;
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                                                                                                                        AAB32904.1;
                                                                                                                                                                               AAA392
                                                                                                                                                                                                              BAA02974.1;
                                                                                                                                                                                                                                                                                                                                                                                          26:231-239(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                  COOPER D.L., DOUGHERTY S.T., DIRKS J.F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Commun. 193:356-363(1993).
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rences between the mouse
                                                                                                                                                                                                                                                                                                                                                                                            RECEPTORS FOR A VARIETY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MACDONALD
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FALSE_NEG
                                                                                                                                                                                                                                                                  There are no rest
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    chain
in the
                                                                                                                                                                                                                                                          Usage
                                                                                                                                                                                                                                                                                                                                                                      IL-2,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gene:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    H.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       mouse IL-2 receptor
                                                                                                                                                                                                                                                                               no restrictions
                                                                                                                                                                                                                                                                                                                                      RECEPTORS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   organization, thymus.";
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                                                                                                                                                                                                                                                           and
                                                                                                                                                                                                                                                                                        EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                       IL-7
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                                                                                                                                                                                                                                                                                             a collaboration -
MBL outstation -
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                                                                                                                                                                                                                                                           commercia.
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Query Match
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CYRG_HUMAN STANDARD,
23.1785;
Q1.-JUL-1993 (Rel. 26, Created)
Q1.-JUL-1993 (Rel. 26, Last sequence update)
15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 37, Last sequence update)
CYTOKINE RECEPTOR COMMON GAMMA CHAIN PRECURSOR (GAMMA-C)
CYTOKINE RECEPTOR COMMON GAMMA CHAIN (P64) (CD132
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MEDLINE; 93293887.
NOGUCHI M., ADELSTEIN
"Characters zation of t
                                                                                                                                   MUNAKATA H., NAKAMURA M., SUGAY "Cloning of the gamma chain of Science 257:379-382(1992).
                                                                                                                                                                                                                                                                                       Homo sapiens (Human)
Eukaryota; Metazoa; (
Futheria; Primates; (
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    interleukin-2
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human
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ANTIGEN).
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J. Biol. Chem. 268:13601-136
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SEQUENCE FROM N.A., AND VARI
MEDLINE: 94004847
PUCK J.M., DESCHENES S.M., P
DISANTO J.P., RIEUX-LAUCAT F., DAUTRY-VARSAT A.,
                                             MEDLINE; 94300093.
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                  VARIANT XSCID ASN-39
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RUSSELL S.M., KKEC
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LEONARD W.J.;
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                                   Immunol. 153:1310-1317(1994)
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ukin-4 receptors studied by molecular
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                                                     growth signaling of mutant IL-2 with X-linked severe combined
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                                                                                NAKAMURA M.,
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SCIDX1.";
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WWW-"http://www.ncbi.nlm.nih.
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morphology.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE; 97295088.
JONES A.M., CLARK P.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STEPHAN V., WAHN V., LE MULLER-FLECKENSTEIN I., DE SAINT BASILE G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             chromosome-linked severe combined immunodeficiency with peripheral
                                                                                                                                                                                                                                                                                                                  VARIANT XSCID CYS
MEDLINE; 98064061
                                                                                                                                                                                                                                                                                                                                                                            "B-cell-negative severe combined common gamma chain mutation."; Hum. Genet. 99:677-680(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     conformation polymorphism analysis.";
Hum. Genet. 96:427-432(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VARIANTS XSCID CYS-226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Proc. Natl.
                                                                                                                                                                                                                                                                         An interleukin-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VARIANT XSCID ARG-115
WEDLINE; 97042245.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      immunodeficiency,";
Invest. 95:895-899(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PEPPER A.E., BUCKLEY R.H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ARIANT XSCID GLN-285.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ARIANT XSCID GLN-
MEDLINE; 95190013
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ARIANT XSCID GLN-HIS-TRP INS-237
AEDLINE; 95164726.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LEVINSKY R.L., KINNON C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Two mucational hotspots
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Defective
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LARK P.A., LESTER T.,
                                                                                                                        SUBUNIT: THE GAMMA CHAIN IS COMMON TO THE IL-2 PROBABLY ALSO THE IL-13 RECEPTORS.
SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
                                      DISEASE: DEFECTS IN 112RG ARE THE CAUSE OF A SEVERE COMBINED IMMUNODEFICIENCY, WHICH IS KNOWN AS AGAMMAGLOBULINEMIA, SWIS OR X-LINKED SEVERE COMBINED IMMUNODEFICIENCY DISEASE (XSCID) SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
SIMILARITY: CONTAINS 1 FIBRONECTIN TYPE III-LIKE DOMAIN DATABASE: NAME-PROW; NOTE-CD guide CD132 entry;
                                                                                                                                                                                                                 FUNCTION:
                                                                                                                                                                                         INTERLEUKINS
                                                                                                                                                                                                                                                                                                                                                                                                                                           A., KINNON C.;
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                                                                                                                                                                                                                                Invest.
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COMMON SUBUNIT FOR THE RECEPTORS
                                                                                                                                                                                                                                                                                                                                     CYS-222
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HORNEFF G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                KATZ F.,
                                                                                                                                                                                                                                                                         gamma
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., SCHROTEN H., FISC
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Best Local S
Matches 72
TISSUE-KIDNEY;
MEDLINE; 97057891.
ZHOU J.F., ZADWORNY
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01-NOV-1997 (Rel. 35, Last sequence update)
15-UUL-1999 (Rel. 38, Last annotation updat
PROLACTIN RECEPTOR PRECURSOR (PRI-R) (TPRIR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PFAM; PF00041; fn3; 1.
PROSITE; PS00241; RECEPTOR_CYTOKINES_1; 1.
PROSITE; PS00340; RECEPTOR_CYTOKINES_2; FALSE_NEG.
Receptor; Transmembrane; Glycoprotein; Signal; Disease mutation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL;
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01-NOV-1997 (Re
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                                                                 SEQUENCE FROM N.A.
                                                                                                          Neognathae;
                                                                                                                          Meleagris gallopavo (Common turkey).
Eukaryota; Metazoa; Chordata; Crania
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(TPRLR).
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Meleagris.
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EMBL; U22947; AAA75038.1; -.
EMBL; U22924; AAA75039.1; -.
HSSP; P16471; 1BP3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  use by non-profit institutions as long as its content modified and this statement is not removed. Usage by ar entities requires a license
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PITTS G.R., YOU S.K., FOSTER D.N., EL HALAWANI K.E.;
Submitted (MAR-1995) to the EMBL/GenBank/DDBJ databases.
FIGURATION: THIS IS A RECEPTOR FOR THE ANTERIOR PITUITARY HORMONE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -:- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
-!- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
-!- SIMILARITY: CONTAINS 4 FIBRONECTIN TYPE III-LIKE DOMAINS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Molecular cloning,
181 QYFGCSFDLTKVKDSSFEQHSVQIMVKDNAGKIKPSFNIVPLTSRVKPDPP-----HIKN
                                                                                                                                                                                                126 OPGSPV-NLTLETORYANIMYLWAKWSPPLLADASSN----HLYHY----ELRLKPEEKE 176
                                                                                  121 PEGDPESAVTELQCIWHNLSYMKCSWI.PGRNTSPDTNYTLYYWHRSLEKIHQCENIFREG
                                                                                                                       EWETVFVG----
                                                                                                                                                           SIE-VPLNERICLQVGSQCSTNE--------SEKPSILVEKCISP 120
                                                                                                                                                                                                                                      QP-:PVTNLSVSVENLCTV--IWT-WNPP--EGASSNCSLWYFSHFGDKQDKKIAPETRR 84
                                               PE-----KPTITKCRSPEKETFTCWWKPGLDGGHPTNYTLLYSKEGEEQVYECPD-YRTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PF00041;
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                                                                                                                                                                                                                                                                           Conservative
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mbrane; Glycoprotein;
                                                                                                                       -VQTQCKINRLNAGMRYVVQVRCMLDPGEWSEWSSERRILISGGLSP
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                                                                                                                                                                                                                                                                                             8.5%;
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                                                                                                                                                                                                                                                                                                                                                                   MW;
                                                                                                                                                                                                                                                                           59;
                                                                                                                                                                                                                                                                                             Score 198.5;
Pred. No. 9.3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Signal; Repeat.
                                                                                                                                                                                                                                                                                                                                                                       CRC32;
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                                                                                                                                                                                                                                                                                                              DB 1;
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PRLR_CHICK
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PIR; JQ1655, JQ1655, HSSP; P16471; 1BP3. 
PFAM; PF00041; fn3; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gallus gallus (Chicken).
Eukaryota; Metazoa; Chord
Neognathae; Galliformes;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ANAKA M., MAEDA K., OKUBO T., NAKASHIMA K.;
Double antenna structure of chicken prolact
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      292
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN. SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROLACTIN.
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PS00340;
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(Rel. 29, Last sequence update)
(Rel. 36, Last annotation update)
(ECEPTOR PRECURSOR (PRL-R) (CPRLP).
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                                                                                                                                                                                                                                                                                                                                                                                                                         RECEPTOR_CYTOKINES_1; 2.
RECEPTOR_CYTOKINES_2; 2.
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rmes; Phasianidae; Phasianinae; Gallus
                                                                                                                                                                                                                                                                                                                                                                                                    Glycoprotein; Signal; Repeat
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                                                                                                            POTENTIAL.
                                                                                                                                                                                                                                                                                        CYTOPLASMIC
                                                                                                                                                                                                                         FIBRONECTIN TYPE-III.
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RESULT 12
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Best Local
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Q95118;
01-NOV-1997 (Rel. 3
01-NOV-1997 (Rel. 3
15-JUL-1998 (Rel. 3
CYTOKINE RECEPTOR C
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CARBOHYD
SEQUENCE
                                                  the
                                                                                                       -i- SUBUNIT: THE GAMMA CHAIN IS COMMON TO THE IL-2, IL-4, IL
PROBABLY ALSO THE IL-13 RECEPPORS.
-i- SUBCELULAR LOCATION: TYPE I MEMBRANE PROTEIN.
-i- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
-i- SIMILARITY: CONTAINS 1 FIBRONECTIN TYPE III-LIKE DOMAIN.
                                                                                                                                                                                                        DNA Cell Biol. 15:453-459(1996).
-!- FUNCTION: COMMON SUBUNIT FOR THE RECEPTORS FOR A VARIETY OF
                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. MEDLINE; 96268473.
                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chorda
Eutheria; Cetartiodactyla;
 entities
                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                           gamma gene."
                                                                                                                                                                                                                                                        YOO J., STONE R.T., SOLINAS-TOLDO S., FRIES R., BEATTIE C.W.; "Cloning and chromosomal mapping of bovine interleukin-2 receptor
                                                                                                                                                                                                                                                                                                                                        Bovinae;
                                                                                                                                                                                                                                                                                                                                                                                       Bos taurus (Bovine).
                                                                                                                                                                                                                                                                                                                                                                                                                01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
CITTOKINE RECEPTOR COMMON GAMMA CHAIN PRECURSOR (GA
(INTERLEUKIN-2 RECEPTOR GAMMA CHAIN) (IL-2R GAMMA
                                                                                                                                                                                                                                                                                                                                                                                                         [L2RG
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                                              European Bioinformatics Institute.
                                                                                                                                                                     INTERLEUKINS.
SUBUNIT: THE GAMMA CHAIN IS COMMON TO THE IL-2,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            YFGCSFDLTKVKDSSFEQHSVQIMVKDNAGKIKPSFNIVPLTSRVKPDPP-----HIKNL
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               non-profit institutions as long as its content and this statement is not removed. Usage by ar
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requires
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335
831 AA;
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335
94102
                                                                                                                                                                                                                                                                                                                                                      Chordata; Craniata; Vertebrata; Mammalia;
actyla; Ruminantia; Pecora; Bovoidea; Bovi
 license
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; Pred. No. 1.1e-07;
59; Mismatches 159;
agreement
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POTENTIAL.
; B977BF07 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    379
(See http://www.isb-sib.ch/announce/
                                              There are no
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                                                                                                                                                                                                                                                                                                                                                                                                                                      (GAMMA-C)
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                                              restrictions
                and for
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               commercial
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Best Local S
Matches 67
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                                                                                                                                                                                                                                                  PRIR_RAT STANDARD; PRT; 610 AA.
P05710; Q63451; Q63723; Q62832; Q64274; Q63479;
O1-NOV-1988 (Rel. 09, Created)
O1-NOV-1997 (Rel. 35, Last sequence update)
O1-NOV-1997 (Rel. 35, Last annotation update)
PROLACTIN RECEPTOR PRECURSOR (PRL-R) (LACTOGEN RECEPTOR).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DOMAIN
DOMAIN
                                                                                         SHIROTA M., BANVILLE D., ALI S., JOLICOEUR C., EDERY M., DJIANE J., KELLY P.A.; "Expression of two forms of prolactin receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
STRAIN-SPRAGUE-DAWLEY; TISSUE-OVARY; MEDLINE; 90241201.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PS00241; RECEPTOR_CYTOKINES_1; 1.
PROSITE; PS00340; RECEPTOR_CYTOKINES_2; FALSE_NEG.
Receptor; Transmembrane; Glycoprotein; Signal.
                               SEQUENCE FROM N.A.
                                                                                                                                        SEQUENCE FROM N.A. MEDLINE; 91155946.
                                                                                                                                                                                        Eutheria;
                                                                                                                                                                                                     Eukaryota;
                                                                                                                                                                                                                      Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TRANSMEM
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                                                                                                                                                                                                                                                                                                                                                                                                                268 PSLFALEAVLIPLGSMGLIVSLICVYCWLER----TMPRIP 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               209
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                                                            Endocrinol.
                                                                                                                                                                                                                                                                                                                                                                                                                                              STLYITMLLIVPVIVAGAIIVLL---LYLKRLKIIIFPPIP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CGHYLFSEGITSGCWFGKKEIR--LYETFVVQLQDPREHRKQPKQMLKLQDLVIPWAPEN 166
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                                                                                                                                                                                        Rodentia;
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                                                                                                                                                                                                       Metazoa;
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                                                              4:1136-1143(1990)
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290
379
256
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81
166
                                (LONG FORM AND SHORT FORM)
                                                                                                                                                                                  Chordata; Craniata; Vertebrata; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8.5%;
23.8%;
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POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 197; DB 1;
Pred. No. 4.4e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CYTOPLASMIC
FIBRONECTIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CYTOKINE RECEPTOR COMMON GAMMA CHAIN.
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                                                                                                                                                                                        Craniata; Vertebrata; Mammalia;
thi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           POTENTIAL.
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TYPE-III.
                                                                                                                                                                                                                                                                                                                                                                                                                                               379
                                                                                                                           BOUTIN J.M.,
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                                                                                                                                            SIGNAL
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EMBL: M57668: AAAA1938.1; -
EMBL: M34093; AAA79273.1; -
EMBL: L48060; AAA79274.1; -
EMBL: U34730; AAA92053.1; -
EMBL: M19304; AAAA1937.1; -
EMBL: M74153; AAAA1937.1; -
EMBL: M74153; AAAA1946.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SHIROTA M., BANVILLE D., DUSANTER-FOURT I., DIANE J., KELLY P.A.; "Cloning and expression of the rat prolactin receptor, a member of the growth hormone/prolactin receptor gene family."; Cell 53:55-77(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -1- SUBCELLULAK LOCATION: TYPE I MEMBRANE
-1- ALTERNATIVE PRODUCTS: DIFFERENT FORMS
SPLICING OF THE PRLR GENE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            the European Bioinformatics Institute. The use by non-profit institutions as long a modified and this statement is not removed. entities requires a license agreement (See )
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       O'NEAL K.D., YU-LEE L.Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. (FORM NB2).
MEDLINE; 95014432.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "A prolactin-dependent i of prolactin receptor."; J. Biol. Chem. 266:20110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 231-610 STOCCO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
-1- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ALI S., PELLIGRINI I.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BANVILLE D., STOCCO R., MURTHY K.K., BOIE Y., KELLY P.A.; Submitted (MAR-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Biochem. Biophys.
                                                                                                                                                                                                                                                                                               FIR; A29884; A29884.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   or send an email to licens@@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE=LYMPHOMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A..
                                                                                                                                                                                                                        PROSITE; PS00340; RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROLACTIN.
                                                                                                                                                                                                                      ps00241; receptor_cytokines_1; ps00241; receptor_cytokines_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            92041834.
                                                                                                                                                                                                    Transmembrane;
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splicing.
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2 1 610
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230 253
254 610
20 117
119 222
31 41
70 81
54 54
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THIS IS A RECEPTOR FOR THE ANTERIOR PITUITARY HORMONE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 266:20110-20117(1991).
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               EXTRACELLULAR (BY SIMI
BY SIMILARITY.
CYTOPLASMIC (BY SIMILA
FIBRONECTIN TYPE-III.
FIBRONECTIN TYPE-III.
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                              PROLACTIN RECEPTOR.
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                                                                                                                                                                                                   Signal;
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ong as its content
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                                                                                                                                                                                                    Repeat;
                                                                                                                               SIMILARITY)
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MBL outstation -
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Best Local Similarity 23.7%;
Matches 68; Conservative
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Q28172;
Q1-NOV-1997
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VARSPLIC
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01-NOV-1997 (Rel. 35, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
PROLACTIN RECEPTOR PRECURSOR (PRL-R)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VARSPLIC VARSPLIC
                                                    SCOTT P., KESSLER M.A., SCHULER L.A.;
"Molecular cloning of the bovine prolactin
of prolactin and growth hormone receptor tr
utero-placental tissues.";
Mol. Cell. Endocrinol. 89:47-58(1992).
-!- FUNCTION: THIS IS A RECEPTOR FOR THE AN
                                                                                                                                                                                     Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata;
Eutheria; Cetartiodactyla; Rur
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                                                                                                                                         SEQUENCE FROM N.A.
TISSUE-ENDOMETRIUM;
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                                                                                                                               MEDLINE; 93246019
                                                                                                                                                                             Bovinae;
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      SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN. SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS. SIMILARITY: CONTAINS 4 FIBRONECTIN TYPE III-LIKE DOMAINS
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                                                                                                                                                                                                                                                                                                                                                                                                                              AKCENPEFERNVENTSCFMVPGVLPDTLNTVRIRVKTNKLCYEDDKLWSNWSQEMSIGKK 339
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MISSING (IN FORM NB2).
V -> A (IN REF. 2).
G -> V (IN REF. 2).
E -> K (IN REF. 1).
Q -> E (IN REF. 2).
A '> G (IN REF. 2).
A '> G (IN REF. 2).
C -> K (IN REF. 2).
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Pred. No. 3.3e-07;
3; Mismatches 120
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KGKSEELLSALGCQDFPPTSDCEDLLVEFL
TGSPSKYKVDLYLALPGGFQKLDNAGELDY
                                                                                                                                                                                                Craniata; Vertebrata; Mammalia;
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EVROLKKTYLWVKWSPPT -> DYRWEVSCHQEALPKSA
KLN (IN SHORT FORM).
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                                                      PITUITARY HORMONE
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                                                                                         distribution fetal and
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between
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and for entities requires a license agreement (See http://www.isb-sib
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL: L02549; AAA51417.1;
HSSP; P14787; 1AN3.
FFAM; PF00041; fn3; 2.
                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
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the European Bioinformatics Institute
       277
                            386 KEMFGDQNDDTLHWKKYDIY -- EKQTKEE
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-----KGFDVHLLEKGKSEE
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                                                                      SQEMSIGKKRNSTLYITMLLIVPVIVAGAIIVLLLYLKRLK-----IIIFPPIPDPGKIF
                                                                                                                          THNVFYVQEAKCENPEFERNVENTSCFMVPGVLPDTLNTVRIRVKTNKLCYEDDKLWSNW
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                                                    SPESSIQIPNDFPVKDTSMWIFVAILSAVICLIMVWAVALKGYSMVTCILPPVPGP-KI-
                                                                                                    THETLKQTQLKIEN--------LYPGQKYLVQIR-----CKPDHGYWSEW
                                                                                                                                                   PEPP--ANLTLELKHPEDRKPYLWIKWSPPTMTDVKSGWFI---IQYEIRLKPEKATDWE
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                                                                                                                                                                                                                                                                                                           Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PS00241;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      email to license@isb-sib.ch).
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nilarity 24.3%;
Conservative 4.
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                                                                                                                                                                                                                                                                                                                                                         WW;
                                                                                                                                                                                                                                                                                             ; Score 186; DB 1;
; Pred. No. 5.3e-07;
44; Mismatches 115
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RRR OCCUPATOR
                                                                                                                                                           RESULT
                                                                                          C1-APR-1990 (Rel. 14, Created)
01-APR-1990 (Rel. 14, Last sequence up
15-JUL-1998 (Rel. 36, Last annotation
                    SEQUENCE FROM N.A.
                                                 Oryctolagus cuniculus (Rabbit).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
                                                                                                                          PRLR_RABIT
                                                                                                                                                 RABIT
                                         Eutheria;
                                                                                  PROLACTIN RECEPTOR
           ISSUE=MAMMARY
MMARY GLAND;
89184578.
                                       Lagomorpha;
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                                                                                  PRECURSOR
                                        Leporidae;
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                                       Oryctolagus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               modified and this statement is not
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*HALABY D., THOREAU E., DJIANE J., MORNON J.P.;

*HOMOlogy_modeling of rabbit prolactin hormone complexed with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DOMAIN
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Proteins 27:459-468(1997)
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PETRIDOU B., BOUTIN J.M., LESUEUR L., KELLY P.A., DJIANE J.;
PETRIDOU B., BOUTIN J.M., LESUEUR L., KELLY P.A., DJIANE J.;
PETRIDOU B., BOUTIN J.M., LESUEUR L., KELLY P.A., DJIANE J.;
PETRIDOU B., BOUTIN J.M., LESUEUR L., KELLY P.A., DJIANE J.;
PETRIDOU B., BOUTIN J., LESUEUR L., KELLY P.A., DJIANE J., LESUEUR J., LE
                                         334 MSIGKKBNSTLY-ITMLLIVPVI--VAGAIIVLLLYLKRLKII--IFPPIPDP 381
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          109 KPSILVEKCISPPEGDPESAVTELQCIWHNLSYMKCSWLPGRNTSPDTNYTLYYWHRSLE 168
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SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
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SIQIPNDETMKDITVMIFVAVLSTIICLIMVMAVALKGYSMVTCIFPPVPGP 274
                                                                                                                                                                                   VFYVQEAKCENPEFERNVENTSCFMVPGVLPDTLNTVRIRVKTNKLCYEDDKLWSNWSQE 333
                                                                                                                                                                                                                                                                                                          PDPPHIKNLSF---HNDD----LYVQWENPQNFISR----CLFYEVEV---NNSQTETHN 273
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27.3%; Pred. No. 6.9e-07;
tive 40; Mismatches 105
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Title: Perfect score: Sequence:

US-09-077-817-4 2324

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SPTREMBL\_11:\*

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199794 seqs, 61255205

Run ğ

protein

protein search, using sw model

Number of Word size Database : Searched: Scoring table:

pass the threshold

sp\_archea:\*

sp\_fungi:\* sp\_bacteria:\*

sp\_invertebrate:\* sp\_human:\*

4

brachydanio

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.
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075462 homo sapien
057519 xenopus lae
Q16564 homo sapien
Q64146 rattus norv
070535 rattus norv
                               Q16386 mustela vis
Q16354 homo sapien
Q921a0 cavia porce
Q63257 rattus norv
P79203 ovis aries
Q18245 caenorhabdi
Q14632 homo sapien
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SEQUENCE
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Submitted (DEC-1996) to the EMBL/GenBank/DDBJ databases
EMBL; U81379; AAD00510.1; -
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                               201 GVLPDTLNTVRIRVKTNKLCYEDDKLWSNWSQEMSIGKKRNSTLYITMLLIVPVIVAGAI
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013221 homo sapien
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092856 homo sapien
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Q09165 caenorhabd1
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sp\_plant:\*
sp\_rodent:\*
sp\_virus:\*

sp\_vertebrate:\*
sp\_unclassified:\*

sp\_phage: \*

sp\_organelle:\* sp\_mhc:\* sp\_mammal:\*

Result

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Best Local Similarity
Matches 295; Conserv
                                                                                                                   Q14633
Q14633;
Q1-NOV-1996
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NON_TER
SEQUENCE
  Homo
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Eukaryota; Metazoa: Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea; Bovi
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097597;
01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-MAY-1999 (TrEMBLrel. 10, Last annotation update)
INTERLEUKIN-13 RECEPTOR ALPHA-1 CHAIN PRECURSOR (FRAGMENT).
                                             01-NOV-1996 (TrEMBLrel.
01-NOV-1996 (TrEMBLrel.
01-NOV-1998 (TrEMBLrel.
INTERLEUKIN-5 RECEPTOR P
                                                                        01-NOV-1998
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"Biological activities of interleukin-13 on bovine lymphocytes:
implications for signaling through IL-13Ral.";
Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.
EMBL, AF074402; AAC98147.1; -
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sapiens (Human):
                                                                                                                                                                                                                                                                                        PSENIVPLTSHVKPDPSHIKNLSFQNGDLYVQWTNPQNFQSQCLCYEVEVINSHAETHDI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PSFNIVPLTSRVKPDPPHIKNLSFHNDDLYVQWENPQNFISRCLFYEVEVNNSQTETHNV 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLQVGSQCSTNESEKPSILVEKCFSPPEGDPESAVTALQCIWHNLRYMKCTWLPGRNASP 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLQVGSQCSTNESEKPSILVEKCISPPEGDPESAVTELQCIWHNLSYMKCSWLPGRNTSP 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VTNLSVSVENLCTIIWTWNPPEGASPNCSLKYFSHFGNKQDKKIAPETHRSKEVPLNERI 60
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39644
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. 01, Last sequence update)
. 08, Last annotation update)
PRECURSOR.
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Pred. No. 3.9e-133;
7; Mismatches 37;
                                                                                                                                                                     PRT;
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Best Local S
Matches 102
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SEQUENCE
 J. Immunol. 10
EMBL; U65747;
                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                      01-NOV-1998 (TERMBLTel. 08, Created)
01-NOV-1998 (TERMBLTel. 08, Last seq
01-NOV-1998 (TERMBLTel. 08, Last ann
IL-13 RECEPTOR ALPHA 2.
                                                                                                                                                                                                                                                                       O88786 PRELIMINARY;
                                                                  COLLINS M.;
                                                                             DONALDSON D.D.,
HENDERSON S.L.,
                                                                                                                        STRAIN-C3H/HEJ;
                                                                                                                                                                                           Mus musculus (Mouse)
                                                                                                                                                                                                                                                             088786
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Eutheria; Primates;
                                      "The murine IL-13 receptor alpha characterization, and comparison
                                                                                                           MEDLINE; 98391042
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              receptor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE=PERIPHERAL BLOOD;
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                                                                                                                                                                                                                                                                                                                                             ICHLWIKLFPPIPAPKSNIKDLFVTTN----
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161:2317-2324(1998).
7; AAC33240.1; -.
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                                                                               WHITTERS M.J., FITZ L., O'HARA R.M. JR., BEIER I
                                                                                                                        TISSUE-THYMUS;
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Pred. No. 6e-18;
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INTERLEUKIN-5 REC
247AB980 CRC32;
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with
                                                    molecular cloning
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                                       murine IL-13
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                                                                               D.R., TURNER
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                                         receptor alpha
                                                                             FINNERTY H
                                                                                                                                                                Mammalia;
Mus.
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                                                                               C.R.,
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Best Local
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SIGNAL
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Eukaryota; Metazoa; Chordata;
Eutheria; Primates; Catarrhini
                                                                                                                                                                                                                                                                                                                                                                                     01-NOV-1996
                                                                                                                                                                                                                                                                                                                                                                                                                     Q14631
                                                                                                                                                                            SEQUENCE
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                                                                                                                                                                                                                       EMBL;
                                                                                                                                                                                                                                            receptor.
                                                                                                                                                                                                                                                     MURATA Y., TAKAKI S., MIGITA M., KIKUCHI Y., TOMINAGA A., TAKATSU K.;
"Molecular cloning and expression of the human interleukin 5
                                                                                                                                                                                                                                                                          TISSUE-PERIPHERAL BLOOD;
MEDLINE; 92121815.
                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                              J1-NOV-1996 (TrEMBLrel. 01, Created)
J1-NOV-1996 (TrEMBLrel. 01, Last sequence update)
J1-NOV-1998 (TrEMBLrel. 08, Last annotation updat
INTERLEUKIN-5 RECEPTOR TYPE 2 PRECURSOR.
              140
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                                                                                                                                                                                                                                Exp.
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                                                                                                 PPVTNLSVSVENLCTVIWTWNP-PEGASSNCSLWYFSHFGDKQDKKIAPETRRSIEVPLN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GYTGPDSK----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              --IGKKRNSTLYITMLLIVPVIVAGAIIVLLLYLKRLKIIIFPPIPDP 381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           YYWHRSLEKIHQCENIFR-EGQYFGCSFDLTKYKDSSFEQHSVQIMVKDNAGKIKPSFNI 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C-TNGSEVQSPWIEASYGISDEGSLETKIQDMKCIYYNWQYLVCSWKPGKTVYSDTNYTM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WKPPVVIEKFKGCTLEYELKYRNVDSDSWKTIITRNLIYKDGFDLNKGIEGKIRTHLSEH 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WNPP-----EGASSNCSLWYFSHFGDKQDKKIAPETRRSIEVPLNE----RICLQVGSQ 101
                                 ESKCVTILHKGFSASVRTILQNDHSLLASSWASAELHAPPGSPGTSIVNLTCTTNTTEDN
                                                      ERICLQV-----GSQCSTNESEKPSILVEKCIS----PPEGDPESAVTELQCIWHNL---
                                                                           PPV-NFTIKVTGLAQVLLQWKPNPDQEQRNVNLEY-----QVKINAPK-EDDYETRIT 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NDMKLKR---RANESEDLCFFV-------RCKVNIYC-ADDGIWSEWSEEECWE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QEAKCENPEFERNVENTSCFMVPGVLPDTLNTVRIRVKTNKLCYEDDKLWSNWSQEMS--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FQLQNIVKPLPPEFLHISVENSIDIRMKWSTPGGPIPPRCYTYEIVIREDDISWESATDK 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VPLTSRVKPDPPHIKNLSFHND-DLYVQWENPQNFI-SRCLFYEVEVNNSQTETHNVFYV 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FFWYEGLDHALQCADYLQHDEKNVGCK--LSNLDSSDYKDFFICVNGSSKLEPIRSSYTV
                                                                                                                                                                                                                       X61177;
                                                                                                                                Similarity
                                                                                                                                                                                                                                Med. 175:341-351(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
 SY---MKCSWLPGRNTSPDTNYTLYYWHRSLEKIHQCENIFRE--GQYFGCSFDL 189
                                                                                                                                                                            396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                       CAA43484.1;
                                                                                                                                                                            AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -IIFIVPVCLFFIFLLLLLCL----IVEKEEPEP
                                                                                                                                                                                       396
                                                                                                                                                                            44998 MW;
                                                                                                                                                                                                                                                                                                                     Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           44483 MW;
                                                                                                                                                                                                 20
                                                                                                                                12.28;
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                                                                                                                      64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 287.5; DB 11
Pred. No. 2.2e-17;
4; Mismatches 156;
                                                                                                                                Score 282.5;
Pred. No. 6.3
                                                                                                                                                                            INTERLEUKIN-5 RECEPTOR 85FBF684 CRC32;
                                                                                                                                                                                                 POTENTIAL
                                                                                                                                                                                                                                                                                                                     Craniata; Ve
i; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
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                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                     396
                                                                                                                                5; DB 4;
5.3e-17;
                                                                                                                                                                                                                                                                                                                               Vertebrata;
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                                                                                                                                           Length
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                                                                                                                                                                                       TYPE
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                                                                                                                      65;
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360
                                                                                                                                                                                                                                                                                     Matches 100;
                                                                                                                                                                                                                                                                                               Query Match
Best Local :
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Q9ZOK4; PRELIMINARY; 11
Q9ZOK4; 10; CTEMBLITE1. 10; CTEMBLITE1. 10; Las.
01-MAY-1999 (TIEMBLITE1. 10; Las.
1NTERLEUKIN.5 RECEPTOR ALPHA PI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  190
                                                                                                                                                                                                                                                                                                                                                               SIGNAL
                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                     CHAIN
                                                                                                                                                                                                                                                                                                                                                                        Signal; Receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                              Worris T.E.
                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                     301
                                                                                      241
                                           300
                                                                 249
                                                                                                           189
                                                                                                                                 181
                                                                                                                                                      135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    364 ICHLWIKLFPPIPAPKSNIKDLFVTTN----
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IIVLLLYLKRLKII----IFPPIPDPGKIFKEMFGDQNDDTLHWKKYDIYEKQTKEETDSV
                                                                                                                                                                                                                                                                                               Similarity
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415 /
                                                                                                                                                                                                                                                                                     Conservative
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                                                                                                                                                                                                                                                                                              12.0%;
                                                                                                                                                                                                                                                                                                                                          46913 MW;
                                                                                                                                                                                                                                                                                     65;
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"Cloning and Characterization of the receptor alpha cDNA.";
Submitted (APR-1996) to the EMBL/GenBEMBL; U55215; AAD09361.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cavia porcellus (Guinea pig).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TETQP------PVTNLSVSVENLCTVIWTWNP-PEGASSNCSLWYFSHFGDKQDKKIAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DDI. TYQWENPQN-FISRCLFYEVEVNNSQTETHNVFYVQEAKCENPEFERNVENTSCFMV
                                                                                                                                                                                                                                                    QYFC.SFDLTKVKDSSFEQHSVQIXVKDNAGKIKPSFNIVPLTSRVKPDPPHIKNLSFHN
                                                                                                                                                                                                                                                                                                                                          -----WENL-SY---MKCSWLPGRNTSPDTNYTLYY----WHRSLEKIHQCENIFRE--G
: || || : |: |: || || || || : |: ::
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ETRRS---IEVPLNERICLQVGSQCSTNESEKPSILVEKCISPPEGDPESAVTELQCI-- 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TKVXDS3FEQHSVQIMVKDNAGKIKPSFNIVPLTSRVKPDPPHIKNLSFHNDDLYVQWEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               YSRLRCYQVSLHCTWLVGTDAPEDTQYFLYYRYGSWTE--ECQEYSKDTLGRNIACWFPR
                                  PGYN:FDTLNTVRIRVKTNKLCYEDDKLWSNWSQEMSIGKKRNSTLYITMLLIVPVIVAGA
                                                                                                   SRLSIQWQKPVSAFPIHCFEYEVKICNTKD-----YYQVEKTTTNAFVSTTDGVSKY--
                                                                                                                                                                                                       RNTACWFFRTFIHSKARDRLAVHVNGSSNHATIKFFDQLFDTQAIDQPNPPMDVTAETEG
                                                                                                                                                                                                                                                                                                          TAASNY !! NLKSYEVSLHCTWLAGKDAPEDTQYFLYYRYGPW-----TEECQEYSKDTLS
                                                                                                                                                                                                                                                                                                                                                                                                                ETRNIQS: CETTLHQGVSASVRTILWHGHSLLASSWVSAEHKAPPGSPGTSIVNLTCTTN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TDTLPDKKFLLLPPINFTIKVTGLAQVVLCWEPNPNQGQKNVNLNYHVKINTPQEEDY--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -- RLKITTEPPIPDPGKTEKEMEGDQNDDTLHWKKYDIYEK 407
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-SIQVRAAVSPHC-RAMGLWSKWSQPVYVGKEKKP--IAGWFLITLTAVLCF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    to the EMBL/GenBank/DDBJ
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 279.5; DB 11;
Pred. No. 1.2e-16;
5; Mismatches 186;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INTERLEUKIN-5 RECEPTOR 99EBCB82 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRECURSOR.
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RESULT
Q14431
ID Q1
AC Q1
DT 0:
DT 0
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Best Local s
Matches 81
                                              Q14431 PRELIMINARY;
Q14431;
Q1-NOV-1996 (TrEMBLrel. (
01-NOV-1996 (TrEMBLrel. (
01-NOV-1998 (TrEMBLrel. (
GM-CSF RECEPTOR.
            Homo
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Q15469;
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SEQUENCE
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SIGNAL
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1996 (TrEMBLrel. 08, Last annotation update)
SOLUBLE INTERLEUKIN-5 RECEPTOR PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE-PERIPHERAL BLOOD;
MEDLINE; 92121815
MURATA Y., TAKAKI S., MIGITA M., KIKUCHI Y., TOMINAGA A., 1
"Molecular cloning and expression of the human interleukin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
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            sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PQN-FISRCLFYEVEVNNSQTETHNVFYVQEAKCENPEFERNVENTSCFMVPGVLPDTLN 308
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PPVTNLSVSVENLCTVIWTWNP-PEGASSNCSLWYFSHFGDKQDKKIAPETRRSIEVPLN 91
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333 AA;
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333 S
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; Pred. No. 2.4e-12;
52; Mismatches 145;
                                                                               Last sequence update)
Last annotation update)
                                                                                                                                                                        Created)
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SOLUBLE INTERLEUKIN-5 RECEPTOR; E86A7792 CRC32;
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Query Match
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Matches |
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Etdsues.";
Endocrinology 138:3187-3194(1997).
EMBL; AF027403; AAB83999.1; -
PFAM; PF00041; fn3; 2.
SEQUENCE 296 AA; 33854 MW; 8B4
                                                                                                                                                                                                                                     Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea; Bovi
                                                                                                                                                                                                                                                                                               01880):
01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
PROLACTIN RECEPTOR SHORT FORM.
                                                                                                        SCHULER L.A., NAGEL R.J., GAO J., "Prolactin receptor heterogeneity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "REFORM THE CONTROL OF THE PREVOT B., NATHAN D.G., SIEF "A functional isoform of the human granulocyte/macrophage colony-stimulating factor receptor has an unusual cytoplasmic domain.";
                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                      Bovinae;
                                                                                                                                                                                                                                                                                                                                                                                                                 018880
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. MEDLINE; 91352066.
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Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                378 IP---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ----DPGKIFKEMFGDQNDDTLHWKKY 402
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Pred. No. 1.4e-11;
75; Mismatches 178;
    8B40CCD8
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                                                                                                           HORSEMAN N.D., in bovine feta
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    CRC32
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                                                                                                             fetal
                                                                                                                                 KESSLER M.A.;
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                                                                                                                                                                                                                                          Bovidae;
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Oreochtomis mossambicus (Mozambique tilapia) (Tilapia mossambica).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Actinopterygii;

Neopterygii; Teleostei; Euteleostei; Acanthopterygii; Percomorpha;

Perciformes; Labroidei; Cichlidae; Tilapia.
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01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-MAY-1999 (TrEMBLrel. 10, Last annotation update)
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                                                                                                                                                           NVENTSCFMVPGVLPDTLNTVRIRVKTNKLCYEDDKLWSNWSQEMSIGKKRNSTLYITM- 349
                                                                                                                                                                                                                                                                QWENPONFISR----CLFYEVEV----NNSQTETH-----NVFYVQEAKCENPEFER
                                                                                                                                                                                                                                                                                                                                                                       TKVKDSSFEQHSVQIMVKDNAGKIKPSFNIVPLTSRVKPDPPHIKNLSFHNDD----LYV 245
                                                                                                                                                                                                                                                                                                                                                                                                                              TEITCRSPEKETFTCWWKPGSDGGLPTTYALYYRKEGSDVVHECPDYHTAGKN-SCFFN- 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SQEMSIGKKRNSTLYITMLLIVPVIVAGAIIVLLLYLKRLK-----IIIFPPIPDP 381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PEPP--ANLTLELKHPEDRKPYLWIKWSPPTMTDVKSGWFI---IQYEIRLKPEKATDWE 181
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AYLHREKSVWILVVVFSAFILIILIWLIQMNSHSLKHCMLPPVPGP
                                                                                                                                                                                                                SWEPPHKADTRSGWITLIYELRVKLEDEESEWENHAAGQQKMFNIFSLRSG------
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                                                    -----KRLKIIIFPPIPDP
                                                                                                                                                                                                                                                                                                                    -KNDTLIWVSYNITVVATNALGKTYSDPVDIDVVYIVKPHPPEKLEVTVMKDQGWPFLRV 149
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                                                                                                         -GTYLIQVR----CKPDHGFWSEWS------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 177; DB 13;
Pred. No. 8.9e-08;
40; Mismatches 104
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41; Mismatches
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CLF-1.
         A1-NOV-1998 (TREMBLIE).
01-NOV-1098 (TREMBLIE).
01-MAY-1999 (TREMBLIE).
CYTOKINE-LIKE FACTOR-1 F
                                                                                                                                                                                                                                                                             272
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SEQUENCE
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Ovis aries (Sheep),
Eukeryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eukeryota; Metazoa; Chordata; Ruminantia; Pecora; Bovoidea; Bovi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             046561
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Long and short forms of the ovine prolactin receptor: cDNA cloning and genomic analysis reveal that the two forms arise by different alternative splicing mechanisms in ruminants and in rodents."; J. Mol. Endocrinol. 19:109-120(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. MEDLINE; 98001468. SIGNON C., BINART N., DJIANE J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-JUY-1378 (TIEMBLIEL 06, Created)
01-JUN-1993 (TIEMBLIEL 06, Last sequence update)
01-MAY-1994 (TIEMBLIEL 10, Last annotation update)
PROLECTIN RECEPTOR LONG FORM PRECURSOR.
                                                                075462;
                                                                             €75462
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                                                                                                                                                                                                                                                                             HNV::YVQEAKCENPEFERNVENTSCFMVPGVLPDTLNTVRIRVKTNKLCYEDDKLWSNWS
                                                                                                                                                                                                                                                                                                         PEPP -- VNLTLELKHPEDRKPYLWIKWSPPTLTDVKSGWFS -- IQYEIRLKPEKATDWET
                                                                                                                                                                                                                                                                                                                                PDF://IIKNLSF---HNDD-----LYVQWENP-----QNFISRCLFYEVEVNNSQT---ET
                                                                                                                                                                                                                                                                                                                                                         TLIHECPD-YKTGGPNSCYF--SKKYTSIWKMYVITVSAINQMGISSSDPLYVDVTYIVE
                                                                                                                                                                                                                                                                                                                                                                                     EKIHQCENIFREGQYFGCSFDLTKVKDSSFEQHSVQIMVKDNAGKIKPSFNIVPLTSRVK 227
                                                                                                                                                                       EMEGDONDDTLHWKKYDIY--
                                                                                                                                                                                                PESETQIPNDEPVKDTSMWIEVGVLSAVICLIMVWAVALKGYSMVTCILPPVPGP-KI--
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581 AA;
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65235
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             PRECURSOR
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                                                                                                                                                                     EKQTKEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    46;
                       Last sequence up
                                                   Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 175; DB 6;
Pred. No. 2.6e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  POTENTIAL.

PROLACTIN RECEPTOR LONG

6792A7C7 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                            291
                                                                                                                                                                       412
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                                                                                                                                                                                                                                                    -LYPGQKYLVQIR---
                                                                             422
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                                                                                                                                                                                                                                                   -CKPDHGYWSEWS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bovidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    , 88
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                                                                                                                                                                                                                                                                              331
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Homo sapiens

(Human)

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RESULT 13
057519
ID 057519
AC 057519
DT 01-UNAY
DT 01-WAY
DE GP130P
GN XGP130P
GN XGP130
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                                                                             Query Match
Best Local Similarity
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Best Local
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057519;
01-JUN-1998
01-JUN-1998
01-MAY-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota;
Eutheria; F
[1]
                                                                                                                                                                                   CHEN J., GRACE A., CHIEN K.R.;
Submitted (JAN-1998) to the EMBL/GenBank/DDBJ
EMBL; AF041845; AAC03531.1; -
PFAM; PF00041; fn3; 4.
SEQUENCE 881 AA; 99003 MW; 647E152E CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Signal.
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J. Immunol. 0:0-0(1998).
EMBL; AF059293; AAC28335.1; -.
                                                                                                                                                                                                                                                                                                                                                                                               Xenopus laevis (African clawed frog).
Eukaryota; Metazoa; Chordata; Craniata; Ve
Batrachia; Anura; Mesobatrachia; Pipoidea;
                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    XGP130.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GP130P1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PFAM; PF00041; fn3; 2.
  123 GDPESAVTELQCIWHNLSYMKCSWLPGRNTSPDTNYTL-YYWHRSLEKIHQCENIFREGQ 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             291
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LLLCAGG----GGGGGGAAPTETQPPVTNLSVSVENLCTVIWTWNPPEGASSNCSLWYFSH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LLLCVLGAPRAGSGAHTAVISPQDPTLLIGSSLLATCSV---HGDPPGATAEGLYWTLN-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        --SNQTSC-RLAGLKPGTVYFVQVRCNPFGI-YGSKKAGIWSEWSHPTAASTPRS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NLSFHNDDLYVQWENP---QNFISRCLF---YEVEVNNSQTETHNVFYVQEAKCENPEFE
| | | | :| :| : | | | :| :|
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PEGDPESAVTELQCIWHNLSYMKCSWLPGRN--TSPDTNYTLYYWHRSLEKIHQCENIFR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RNVENTSCFMVPGVLPDTLNTVRIRVKTNKLCYEDDK--LWSNWSQEMSIGKKRN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RVGGLEDQLSVRWVSPPALKDFLFQAKYQIRYRVEDSVDWKVVDDV--------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VGPH-SCHIP----KDLALFTPYEIWVEATNRLGSARSDVLTLDILDVVTTDPPPDVHVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EGQYFGCSFDLTKVKD-SSFEQHSVQIMVKDNAGKIKPSFNIVPLTSRVKPDPP---HIK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -VGLPPEKPVNISCWSKNMKDLTCRWTPGAHGETFLHTNYSLKYKLRWYGQDNTCEEYHT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ----GRRLPPELSRYLNA---STLALANLNGSRQRSGDNLVCHARDGSILAGSCLY-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FGDKQDKKIAPETRRSIEVPLNERICLQV----GSQCSTNE-----SEKPSILVEKCISP 120
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Similarity 22.5%;
80; Conservative 5
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422 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (TrEMBLrel. 06, Created)
(TrEMBLrel. 06, Last sequence update)
(TrEMBLrel. 10, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                               99003 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   46301 MW;
                                                                             7.18; 25.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    53;
                                                       32;
                                                    Score 164; DB 13;
Pred. No. 4.1e-06;
32; Mismatches 81;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 169.5; DB 4; Length 422; Pred. No. 5.2e-07;
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CYTOKINE-LIKE FACTOR-1.
; 877F9BC9 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            881
                                                                                                                                                                                                                                                                                                                                                                                                 Vertebrata;
ea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ₿
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                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                 Amphibia;
Xenopodinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    63;
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                                                    Gaps
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Best Local Similarity
"atches 65; Conserv
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RAINES M.A., LIU L., QUAN S.G., JOE V., DIPERSIO J.F., GOLDE D.W.;

"Identification and molecular cloning of a soluble human
granulocyte-macrophage colony-stimulating factor receptor.";

Proc. Natl. Acad. Sci. U.S.A. 88:8203-8207(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Aomo sapiens (Human).
Aomo sapiens (Human).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Entheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Cloning of a potentially soluble receptor for Nucleic Acids Res. 18:7178-7178(1990).

EMBL; M7832; AAA35909.1; -.

EMBL; X54935; CAA38697.1; -.

Signal; Alternative splicing.

SIGNAL: 1 22 POTENTIAL.

CHAIN 23 333 GM-CSF RECEPTOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q16564 PRELIMINARY;
Q16564;
Q1-NOV-1996 (TrEMBLrel. 01,
Q1-NOV-1996 (TrEMBLrel. 01,
Q1-NOV-1998 (TrEMBLrel. 08,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ASHWORTH A., KRAFT A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE; 91088339.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE-PLACENTA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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256
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   31 TOPPUTNLSVSVENLCTVIWTWNPPEGAS-SNCSLWYFSHFGDKQDKKIAPETRRSIEVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                   29 TVAPASSLNVRFDSR-TMNLSWDCQENTTFSKCFL----TDKKNRVVEPRLSNNECSC
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                                                                                                                                                                                                                                                                                                                                                                    LNERICLQVGSQCSTNESEKPSILVEKCISPPEGDPESAVTELQCIWHNLSYMKCSWLPG
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                                                    EVN - - NSQTETHNVFYVQEAKCENPEFERNVENTSCFMVPGVLPDTLNTVRTRVKTNKLC
                                                                                                         GTSREIGIQFFDSLLDTKKIERFNPPSNVTVRCNTTHCLVRWKQPRTYQKLSYLDFQYQL
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GM-CSF RECEPTOR

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STRAIN-WISTAR; TISSUE-BRAIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPEL K., BUTTINI M., SAUTER A., GEBICKE-HAERTER P.J.; "Cloning of rat interleukin-3 receptor beta-subunit from cultured microglia and its mRNA expression in vivo.";
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Eukaryota; Metazoa; Chor
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11-NOV-1996 (TrEMBLrel. 01, Last sequence update)
11-NOV-1998 (TrEMBLrel. 08, Last annotation update)
.NTERLEUKIN-3 RECEPTOR BETA-SUBUNIT (FRAGMENT).
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                              KRNSTLYITMLLIVPVIVAGAIIVLLLYL------KRLKIIIFPPIPDPGK 383
                                                                                         ---CENPEFERNVENTSCFMVPGVLPDTLNTVRIRVKTNKLCYEDDKLWSNWSQEMSIGK 338
                                                                                                                        --HIQMNPPTL-NLTKNRDSYSLHWETQK------MSYPFIQHAFQVQYKKK 382
                                                                                                                                                      TSRVKPDPPHIKNLSFHNDDLYVQWENPQNFISRCLFYEVEVNNSQTETHNVFYVQEAK- 282
                                                                                                                                                                                     AGEKKCSPVVKELQASRYTRYHCSLNVS--DPAAHSQYTVSVK-RLEQGKFIESFN----
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                                                                                                                                                                                                                                                                                                                                          TWNPPEGASS--NCSLWYFSHFGDKQDKKIAPETRRSIEVPLNERICLQVGSQCSTNESE 108
                                                           LDRWEDSKTE-NLNHAHSMDLPQLEPGTSYCARVRVKT---IPEYKGLWSEWSNECTW--
-TIDWYMPTLWIVLILVELILTFLLALREGCIYGCKLYRRWK----EKIPNPSK 485
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

EFFETURE  REFYTTION LUTSION LUTSION VERSION VE	RUSULT	0 00 000 000 000 000 000 000 000 000 0
A63257 4009 bp DNA N Sequence 3 from Patent W09720926. A67257 o571708 A6725-1 GI:3717098  unidentified. unidentified unidentified. I 'bases 1 to 4009) Caput, D., Ferrara, F., Laurent, P., Vita II-13 XECEPTOR POLYPEPTIDE Patent: W0 9720926-A 3 12-JUN-1997; SANOII 3A [FR] O.Ker publication FR 2742156 19970627 Other publication FR 2742156 19970613.	ALIGNMENTS	4009 100.0 4009 5 A63257 3999 99.8 3999 9 HSIL13RA 1697 4039 9 HSIL13RA 1697 2.3 1708 41 HSU62858 976.6 1572 11 HSU62858 976.6 1572 11 HSU62858 976.6 24.4 1048 3 AF974402 281.8 7.0 458 13 G29644 281.8 7.0 458 13 G29644 281.8 7.0 1487 33 HSU674642 253.6 6.3 141857 42 AC010532 251.4 6.3 152078 33 HSU574642 251.4 6.3 152079 3 AP000017 250 6.2 151116 9 AP00017 250 6.2 151116 9 AP000113 250 6.2 1813451 11 HSAC000118 249.8 6.2 1846213 11 HSAC000118 249.2 6.2 183451 11 AC004953 249.2 6.2 183451 11 AC004953 249.2 6.2 183451 11 AC004953 249.2 6.2 1217040 42 AC008623 240.2 6.2 121829 9 HSPEX 247.6 6.2 221825 9 HSPEX 247.6 6.2 123339 43 AC011542 247.6 6.2 123339 43 AC004065 246.4 6.1 129557 11 AC004008 246.5 6.1 1195561 33 HSAC000406 246.6 6.1 119557 11 AC002574 245.8 6.1 155081 33 HSAC000406 245.8 6.1 155081 33 HSAC000756 245.6 6.1 155081 10 HSS37814 245.6 6.1 155081 10 HSS37816 245.6 6.1 122948 10 HSS91H21
PAT 12-MAR-1998		A63257 Sequence 3 Y09328 H.sapiens m Y10659 H.sapiens m Y10659 H.sapiens I U81379 Homo sapien U81379 Homo sapien U62858 Human inter S80963 NR4=IL-13 r U81380 Human inter S80963 NR4=IL-13 r U81380 Human inter AF074402 Bos tauru G29644 human S7S S ACC04482 Homo sapi AL105458 Homo sapi AL105458 Homo sapi AL109953 Homo sapi AL109953 Homo sapi AP000117 Homo sapi AP000119 Homo sapi AP000113 Homo sapi AP000313 Homo sapi AC000118 Human BAC AC0004953 Homo sapi AC0004953 Homo sapi AC001522 Homo sapi AC001522 Homo sapi AC001522 Homo sapi AC001542 Homo sapi AC001542 Homo sapi AC001542 Homo sapi AC001542 Homo sapi AC001544 Homo sapi AC001549 Homo sapi AC011541 Homo sapi AC011238 Homo sapi AC011238 Homo sapi AC012549 Homo sapi AC012549 Homo sapi AC004659 Homo sapi AC004659 Homo sapi AC004659 Homo sapi AC012549 Homo sapi AC012549 Homo sapi AC004549 Homo sapi AC002549 Homo sapi AC003549 Homo sapi

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Submitted (20-JAN-1997) J-F.M. Gauchat, Geneva Biomedical Research Institute, Immunology, Glaxo, Research And Development, 14 Ch Des Aulx, Plan-Les-Ouates, CH1288, SWITZERLAND
Location/Qualifiers
1. 4039
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 4039)
Gauchat, J.F.M., Schlagenhauf, E., Feng, N.P., Moser, R., Yamage, M., Jeannin, P., Alouani, S., Elson, G., Notarangelo, L.D., Wells, T., Eugster, H.P. and Bonnefoy, J.Y.
A novel 4 kb IL-13Ra mRNA expressed in human B, T and endothelial cells, encoding for an alternate type two IL-4/IL-13R
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On Sep 13, 1999 this sequence version replaced
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ivpltsrykpdpphiknlsehnddlyvqmenponfisrclfyevevnnsqtethnyfy 

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1 (bases 1 to 1572)
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/function="cytokine receptor"
/note="IL-13 receptor: IL-13R or IL-13Ralpha; this protein together with the 140 kDa II-4 binding protein, IL-4R or IL-4Ralpha, can form a functional receptor for IL-13; IL-13R plus IL-4R is also one of the functional forms of the IL-4 receptor, the other is I!-4R plus the common cytokine receptor gamma chain"
                                                                                                                                                                                  /product="interleukin-13 receptor"
/protein_id="AAB37127.1"
/db_xref="pib:9169876"
/db_xref="GI:1695876"
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Location/Qualifiers
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Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; l
1 (bases 1 to 1680)
Hilton,D.J., Zhang,J.G., Metcalf,D., Alexander,W.S.,
and Willson,T.A.
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/codon_start=1
/codon_start=1
/product="IL-13 receptor alpha chain"
/product="IL-13 receptor alpha chain"
/protein_id="AaB50695.1"
/db_xref="plb_19911504"
/db_xref="gl:1911504"
/db_xref="gl:1911504"
/translation="MARPALLGELLVILLWTATVGOVAAATEVOPPVTNLSVSVENLC
TILWTWSPPEGASPUCTLRYFSHFDDQODKKIAPETHRKEELPLDEKICLQVUSQCSA
NESEKPSPLVKKCISPPEGDPEGAVTELKCIWHINLSVHKCSWLPGRWTSPDTHYTLYV
WYSSLEKSROCENIYREOQHIACSFKLTKVEPSFEHONVQIMVKDNAGKIRPSCKIVS
LTSYVKPDPPHIKHLLLKNGALLVQWKNPQNFRSRCLTYSTENNUTQTDTRHNILEVEE
DKCQNSESDRNMEGTSCCDLPGYLADAVTTURVRVKTNKLCEDDNKLWSDWSEAQSIG
KEONSTFYTMLLTIPVEVAVAVIILLFYLKRLKIIIFPPIPDPGKIFKEMFGDQNDD
TLHWKKYDIYEKOSKEETDSVVLIENLKKAAP"
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61. .1335
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61. .1335
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Submitted (24-JUN-1999) Biochemistry, Kyusha Medicine, Maidashi, Fukuoka 812-82, Japan Sequence update by submitter
On Jun 24, 1999 this sequence version replace
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/trans1atlon="memparlogum.llcaggggggggaaptetqppvtnlsysyen
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STNSSEKPSILVEKCISPPEGDPESAVTELQCIWHNLSYMKCSWLPGRNTSPDTNYTL
YYWHRSLEKIHQCENIFREGQYFGCSFDLTKVKDSSFEQHSVQLMVKDNAGKIKPSFN
IVPLTSRVKPDPPHIKNLSFHNDDLYVQWENPQNFISRCLFYEVEVNNSQTETHNVFY
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/protein_id="AAD00511.2"
/db_xref="PID:95174768"
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/db_xref="taxon:9606"
41. .880
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3est Local Similarity

Matches 904; Conserv
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GATAAGAAATTGCTCCAGAAACTCATCGTTCAAAAGAAGTGCCCCTGAACGAGAGGGATC
                   gataagaaaatagctccggaaactcgtcgttcaatagaagtacccctgaatgagaggatt
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Submitted (25-JUN-1998)
Missouri-Columbia, W213
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished
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HNLRYMKCTWLPGRNASPDPNYILYTWHNSLKFSILQCEMY RREGQHIACSFNLTKYKN
SSFEQHSVQVMVRDNAGKISPSFNIVYBLTSHVKPDPSHIKNLSFQNGDLYVQWTNPQN
SOSOCLCYEVPUNSHAETHDIFYVEEAKCQNTEFEGNLEGTICFMVPGVLPDTLNTV
RIRVKNKLCYEDDKLWSNWSQAMSIGQKANQTFYITTLLIIPVIVAAAVIVLLLYLK
                                                                                                                                                                                                                                                              RLKIIIFPPIPDPGK"
227 c 216
                                                                                                                                                                                                                                                                                                                                                                                          /product="interleukin-13
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/db_xref="PID:g4063013"
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/db_xref="taxon:9913"
/cell_type="aortic end
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                                STS; STS
                                         G29644.1
                                                    g1593195
                                                              G29644
                                                                       human STS
                                                                                G29644
 Eukaryota;
                     numan
           sapiens
                               sequence;
                            GI:1593195
sequence; primer;
                                                                     458 bp
SHGC-34461,
 Metazoa;
Chordata;
                                                                    sequence tagged
                                                                                DNA
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                               sequence
 Craniata;
                            tagged
                                                                     SIS.
 Vertebrata;
                               site
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 Mammalia;
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Best Local Similarity 96.6%;
Matches 310; Conservative .**
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                        cctatccycacaacatatccgtatatatcccctctactcttacttccccccaaatttaaag 3036
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AGUCAGCUAGCCAAGGCTCTGTTTATGCTTTTGGGGGGGCATATATTGGGTTCCATTCTCA 65
                                                                                               Prepared with primer pairs provided by Sandoz,
-- Washington University/Merck EST sequence.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Primer A: TCTGTTTATGCTTTTGGGGG
Primer B: GAAATGCCTCTCATTTCCCA
STS 612e: 138
FGR Profile:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: myers@shgc.stanford.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Myers, R.M.
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/map="x"
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Taq Polymerase:
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nes 299; Conservative
 CTACTCAGGAGGCTGÁGGCAGGAGAATTGCTTGAACCTGGGAGGCGGAGGTTGCAGTGAG 12213
                 ctactcgggaagctgaagcaggtgaattgtttgaacctgggaggtggaggttgcagtgag 2055
                                                             CCGTCTCTACTAAAAATACAAAAATTAGCTGGGCATGGTGGCAGGTGCCTGTAATCCCAG
                                                                               tcctctctactaaaactacaaaattaactgggtgtggtggcgcgtgcctgtaatcccag 1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (12-JUN-1998) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Direct Submission
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/db_xref="taxon:9606"
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rimates; Catarrhini; Hominidae; Homo.
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6909: gap of unknown length
17944: contig of 11035 bp in length
17961: gap of unknown length
34519: contig of 16558 bp in length
34536: gap of unknown length
134578: contig of 100042 bp in length.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (15-SEP-1999) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    * NOTE: This is
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DOE Joint Genome Institute
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DOE Joint Genome Institute.
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Ouery Match 6.3%, Best Local Similarity 84.1%;	90008					* 86467 87876 *	* 84747 86466	* 82114 84746	* 80158 82113:	* 78870 80157:	* 76909 78869:	* 75449 76908	* 73777 75448:	* 72331 73776:	* 70472 72330:	69281 70471:	* 57768 69280:	o 66593 67767:	* 64632 66592:	* 63340 64631	* 61385 63339	* 59161 61384	* 56900 59160:	* 55407 56899:	* 54008 · 55406	* 32992 54007:	* ± ±1601. 52991:	* 50567 51600:	* 49120 50566:	* 47481 49119	* 45682 47480:	* 44182 45681:	* 43018 44181	* 41931 43017:	40856 41930:
; Score 253.6; DB 42; Length 141857; ; Pred. No. 4.1e-52;	contig of 2900 pp in length	gap of unknown length	contig of 2197	gap of unknown length	gap of unknown length	gap of unknown	gap of unknown	gap of unknown contig of 2633	gap of unknown leng contig of 1956 bp i	gap of unknown length contig of 1288 bp in	gap of unknown length contig of 1961 bp in 1	contig of 1460 k	gap of unknown lengt contig of 1672 bp in	gap of unknown I	contig of 1859 bp in	contig of 1191 bp in	contig of 1513 h	contig of 1175 bp in length	contig of 1961 k	gap of unknown contig of 1292	contig of 1955 bp in	contig of 2224 bp i	contig of 2261 bp in	contig of 1493 bp	contig of 1399 bp in	contig of 1016 bp 1	contig of 1391 l	contig of 1034 bp in	contig of 1447 bp in	conti	contig of 1799 k	gap of unknown rengulations of 1500 bp in	contig of 1164 bp in	gap of unknown l	gap of unknown l

    

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KEYWORDS
SOURCE
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Contig 18: length 12176 bp
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Contig 9: length 3871 bp
Contig 19: length 3871 bp
Contig 13: length 3497 bp
Contig 16: length 8271 bp
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Contig 15: length 6125 bp
Contig 16: length 3199 bp
Contig 17: length 37805 bp
Contig 17: length 3319 bp
Contig 20: length 3317 bp
Contig 20: length 3318 bp
Contig 8: length 13378 bp
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191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.f)
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the finished sequence as soon as it is available accession number will be preserved.
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TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 278;
          Submitted (29-SEP-1999) Wellcome Trust Genome Campus, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquires:
humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
on Sep 28, 1999 this sequence version replaced 9:5918360.
                                                                                                                               Eukaryota; Metazoa;
Eutheria; Primates;
                                                                                                                                                                                                                                                                                                  HS785G19
 IMPORTANT:
                                                                                  Direct Submission
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software (G. Schuler)"
1 30991 c 30060 g 49313 t
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software (G. Schuler)"
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/note="matching EMBL:AA030054; Identified using the e-PCR
software (G. Schuler)"
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1999 this sequence version replaced gi:5918360. This sequence is unfinished and does not necessarily
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Catarrhini; Hominida
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Pred. No. 4.8e.
0; Mismatches
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20 clone dJ785G19, V
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RESULT 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length: 132647 bp.

* NOTE: This is a 'working draft' sequence

* This record will be updated with the finished sequence

* as soon as it is available and the accession number will
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Cambridgeshire, CB10 1SA, UK. E-mail enquires: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 152878)
                                                                                                                                                                                                                                                                                                             Homo sapiens chromosome in unordered pieces.
                                           Submitted (08-OCT-1999) Wellcome Trust Genome Campus, Hinxton,
                                                                                                                                                                              Homo sapiens
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HTG: HTGS_PHASE1.
                                                                       Direct Submission
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1. .132647
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/chromosome="20"
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28698 c 29621 g 36292
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Pred. No. 6.5e-52;
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20 clone dJ746H2,
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DRAFT SEQUENCE,
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Best Local Similarity
Matches 279; Conserv
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* NOTE: This is a 'working draft' sequence.

* This record will be updated with the finished sequence as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                              aaaactacaaaaattaactgggtggtggtggcgcgtgctgtaatcccagctactcgggaa 2006
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                                                                                                                                                                                                                         in unordered pieces.
AL117352
Submitted (30-SEP-1999) Wellcome Trust Genome Campus, Cambridgeshire, CB10 1SA, UK. E-mail enquires:
                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                           HIG;
                                        Direct Submission
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/db_xref="taxon:9606"
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85.8%;
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Pred. No. 1.5e-51;
0; Mismatches 46
                                                                                                                                                                                                                                                                     DNA HTG 30-SEP-1999
1 clone dJ876B10, WORKING DRAFT SEQUENCE,
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Best Local Similarity
Matches 276; Conserv
49661 AAAACAAAAAAAAAAA 49677
                                                                                                                             49361 TGGACCGGGCACGCTGACGCCTGTAATCCCAGCACTTTGGAAGGCCGAGGCGGGCA 49420
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                                             2125 aaaacaaaacaaaaaa 2141
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Louis acc-AL117352 Length:
Contig_ID: 02199 acc-Arii
* NOTE: This
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represent the correct sequence.
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Search completed: January 20, 2000, 05:08:04 Job time: 9331 sec

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BSSL/CEL Gene. DNA Serglycin - proteo AP2 sequence obtd.

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Number of hits that pass the threshold
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                                                                                                                                                                                                                                                                                                                                                                         consistences, which are receptors for interleukin-13 (IL-13) alpha receptor. The invention relates to new purified peptides comprising 380 or 427 amino control sequences, which are receptors for interleukin-13 (IL-13); the 380 cm. 427 aa proteins are designated IL-13R beta and alpha respectively. The IL-13R beta has high affinity for IL-13R beta and alpha respectively. Such acquires high affinity when associated with the IL-4 cm ceptor. Nucleic acids encoding IL-13R beta and alpha are used as CC diagnostic probes to identify aberrant synthesis or genetic anomalies control as loss of heterozygosity and rearrangements, or chromosomal control as loss of heterozygosity and rearrangements, or chromosomal control as loss of heterozygosity and rearrangements, or chromosomal control as a loss of heterozygosity and rearrangements, or chromosomal control as loss of heterozygosity and rearrangements, or chromosomal control as loss of heterozygosity and rearrangements, or chromosomal control and alpha which can be used for production of recombinant IL-13R beta and alpha which can be used as IL-13 antagonists, specifically to contain the complete responses for treatment of inflammation and control in the production of IL-13. receptors are also useful as antisense molecules for gene continuoussays) to diagnose diseases associated with abnormal expression of IL-13 receptors, when coupled to a toxin also for treatment of overproduction of IL-13R. Cells that express IL-13R at the surface are used to identify ligands and modulators of IL-13R.

Sequence 4:09 BP; 1137 A; 826 C; 882 G; 1164 T;
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Caput D, Ferrara P, Laurent P, Vita N;
WPI; 97-319773/29.
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T85827;
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New purified human interleukin-13 receptors - and related nucleic acids, useful for diagnosis and treatment of inflammation, allerg
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Interleukin-13 receptor; diagnosis; inflammation; allergy; IL-13; ss
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22-DEC-1995; AU-007276.
09-SEP-1996; AU-007270.
09-SEP-1996; AU-007270.
PARTAP DEFRATIONS PHILTON DJ. MRECORIF D, NI
WPI, 97-259018/23.
DNA encoding animal haemopoletin receptor which interacts with interleukin-13 - useful to treat asthma, allergy or condition exacerbated by JgE production

Claim 6; Page 52-54, 93pp; English.

Claim 6; Page 52-54, 93pp; English.

DNA sequences (T66164 and T66165) respectively code for novel mouse and human haemoprotein receptors (M09821 and W09822) designated NR4 that comprise the interleukin-13 (IL-13) receptor alpha-chain. A human bone marrow cDNA libgary was screened with probes comprising nucleotides 82-840 and 840-1270 of murine NR4 cDNA, and a composite sequence for human NR4 was produced from isolated clones. The
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Matches 1348; Conservative
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Sequence 1383 BP; 421 A; 292 C; 319 G; 351 T;
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101-MAX-1997.
23-OCT-1995; AU-006135.
22-DEC-1995; AU-006135.
22-DEC-1995; AU-006135.
22-DEC-1995; AU-007276.
R 09-SEP-1995; AU-007276.
R (AMIX-) AMRAD OPERATIONS PTY LTD.
I H11-ton DJ Metcalf D, Nicola NA, Willson T, Zha.
R (AMIX-) AMRAD OPERATIONS PTY LTD.
I H11-ton DJ Metcalf D, Nicola NA, Willson T, Zha.
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I H11-ton DJ Metcalf D, Nicola NA, Willson T, Zha.
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NR4; haemoprotein receptor; interleukin-13 recepto
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Sequence 1383 BP; 416 A; 296 C; 315 G; 350 T;
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0; Mismatches 247;
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                                                                                                                                                                     03-OCT-1997; U18007.
04-OCT-1996; US-726337.
(GEMY) "EXHETICS INST INC.
Agostino MJ. Jacobs K, Lava
Racie LA, Spaulding V, Trea
Nucleic acids encoding novel secreted proteins - useful as, e.g. anti-infiammatory, immuno-stimulatory or suppressing agents Claim 45: Page 80-81; IlOpp; English.
The sequence is that of an isolated polynucleotide which may be of use in the production of therapeutic compositions for treating or smeliorating a medical condition in a mammal. Such compositions may be used for, e.g. research purposes as markers for tissues, molecular weight markers for gels, primers or probes, for insurstion as carbon, nitrogen or carbohydrate source. They can also used as a cytokine for cell proliferation and differentiation activi
                                                                                                                                                                                                                                                                                                                                                 Homo sapiens adult placenta clone DA136_11 internal coding region adult; placenta; cDNA library; clone DA136_11; anti-inflammatory; therapeutic composition; autoimmune disease; immune; stimulation; suppression; ds.
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DB; 758987
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RESULT V89658
ID V89658
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Homo sapiens.

W09843436-A2.
15-OCT-1998: U06955.
10-APR-1997; US-838821.
(GEMY ) GENETICS INST INC.
Agostino MJ, Jacobs K, Lavallie ER, M.
Racie LA, Spaulding V, Treacy M;
WPI; 99-070077/06.
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Best Local S
Matches 592
                                                                                                                                                                                                          15-FEB-1999 (first entry)
EST clone DA136.
Human; secreted protein; expressed sequence tag; EST; haematopoiesis; tissue growth; activin; inhibin; chemotaxis; chemokinesis; haemostatic; receptor; ligand; thrombolytic; anti-inflammatory; cadherin; anti-tumou
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Sequence 592 BP; 197 A; 121 C; 105 G; 169 T;
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PS Claim 1; Page 288; Si8pp: English.

CC The present sequence represents a human expressed sequence tag (EST).

CC The present sequence represents a human expressed sequence tag (EST).

CC The polynucleotide, which is a secreted EST, and the encoded protein conditions in human and animals altivities which would make conditions in humans and animals, although no supporting data is conditions in humans and animals, although no supporting data is conditions in humans and animals, although no supporting data is conditions in humans and animals, although no supporting data is conditions in suppressing activity, haematopoiesis regulating conditivity, tissue growth activity, activin/inhibin activity, chemotactic/chemokinetic activity, activin/inhibin activity, cativity, thaemostatic and thrombolytic activity, respector/ligand activity, haematopoiesis regulation conditions in vasion suppressor activity, tumour inhibition conditions in vasion suppressor activity, tumour inhibition conditions in vasion suppressor activity, tumour inhibition conditions in vasion suppressor activity.

Sequence 391 BP; 127 A; 82 C; 75 G; 107 T;
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Matches 362
                                                                                     W09814576-A2.
09-ARR-1998.
03-OCT-1997; U18007.
04-OCT-1996; US-726237.
(GEMY ) GENETICS INST INC.
AGOSTINO MJ, Jacobs K, Lavallie ER
Racie LA, Spaulding V, Treacy M;
WPI, 98-240082/21.
Nucleic acids encoding novel secreted anti-inflammatory, immuno-stimulatory Claim 45; Paye 80; 110pp; English.
                                                                                                                                                                                                                                                                                                                                                             Homo sapiens adult placenta clone DA136_11 5' region. adult; placenta; cDNA library; clone DA136_11; anti-itherapeutic composition; autoimmune disease; immune;
                                                                                                                                                                                                                                                                                                                       suppression;
Homo sapiens.
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Sequence 340 BP; 101 A; 73 C; 79 G; 85 T;
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Best Local Similarity
Matches 337; Conserv
                               Nucleic acids encoding novel secreted proteins - useful as, e.g. anti-inflammatory, immuno-stimulatory or suppressing agents Claim 45; Page 82; 110pp; English.

The sequence is that of an isolated polynucleotide which may be of use in the production of therapeutic compositions for treating or ameliorating a medical condition in a mammal. Such compositions may be used for, e.g. research purposes as markers tissues, molecular weight markers for gels, primers or probes, for the production of the production of the production in a mammal.
                                                                                                                                                                                             (GEMY ) GENETICS INST INC.

Agostino MJ. Jacobs K, Lavallie ER, Mccoy JM, Merberg Racie LA, Spaulding V, Treacy M;
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03-OCT-1997; U18007.
04-OCT-1996; US-726237.
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                                                                                                                                                                                        98-240082/21.
                                                                                                                                                                                                                                                                                                                                                                            sapiens adult placenta clone DA136_11 3' region.
t; placenta; cDNA library; clone DA136_11; anti-inflammatory;
apeutic composition; autoimmune disease; immune; stimulation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gactgagcttcaatgcatttggcacaacctgagctacatg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cctgaatgagaggatttgtctgcaagtggggtcccagtgtagcaccaatgagagtgagaa
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nitrogen or carbohydrate source. They can also be or cell proliferation and differentiation activity.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 336.4;
Pred. No. 9.4e
0; Mismatches
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nes 3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 W W B B B B
CC daim 1; Page 1252; 2245pp; Japanese.

CC A single-stranded DNA (or its complementary strand or the corresp.

CC double-stranded DNA) which comprises one of the 7837 "GS" sequences

CC given in T19001-T26837 and which is able to hybridise to part of

CC human genomic DNA, cDNA or mRNA is claimed. The GS (Gene Signature)

CC sequences were obtained from 3'-directed cDNA ilbraries prepared

CC 1'-cend of mRNA by using poly(T) as the sole primer. Since the 3'-

CC untranslated sequence is unique to a particular mRNA species, almost

CC all the 3'-oriented cDNAs hybridise with specific mRNAs. Each ilbrary

CC ils constructed so as to reflect accurately the relative abundance of

CC different mRNAs in the particular tissue from which it was derived.

CC The appearance frequency of a given GS in a CDNA library can be

CC sequences) as a means of diagnosing abnormal cell function or for

CC sequences as a means of diagnosing abnormal cell function or for

CC sequences 265 BP; 56 A; 50 C; 59 G; 91 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  systemic lupus erythematosus, to regulate haematopoiesis, for growth, as an activator or inhibitor, or as a chemotactic or chemokinetic, haemostatic and thrombocytic, receptor/ligand, anti-inflammatory or tumour inhibitor agents.

Sequence 285 BP; 93 A; 36 C; 50 G; 98 T;
                                                                                                                                                                                                                                                                                                               Matsubara
WPI; 95-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                as immune stimulants or suppressors, e.g. for infections, for autoimmune diseases such as systemic lupus crythematosus, to regulate has
                                                                                                                                                                                                                                                                                                                                                                                                                  Fomo sapiens.
FO9514772-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human gene signature
Gene signature; messe
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Identifying gene signatures in 3'-directed human cDNA library for diagnosis of abnormal cell function, by preparing cDNA the reflects relative abundance of corresp. mRNA in specific human
                                                                                                                                                                                                                                                                                                                                                                                       11-JUN-1995.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 cell typing; abnormal cell function; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             cloning; mapping;
                                                                                                                                                                                                                                                                                                                                              OKUBO
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JP-355504.
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                                                                                                                                                                                                                                                                                                                              Okubo K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            messenger RNA; mRNA;
mapping; non-biased
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as multiple sclerosis
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propersise protein (1A7pp; English.

CC This sequence encodes the human HIAP-1 protein, which is a inhibitor of CC apoptosis protein (IAP), and can be used in the method of the invention. CC apoptosis protein (IAP), and can be used in the method of the invention. CC apoptosis protein (IAP), and can be used in the method of the invention. CC proliferative disease by treatment with a compound that inhibits compounds are used to treat proliferative diseases, specially cancers of compounds are used to treat proliferative diseases, specially cancers of cretum, cervix or endometrium, particularly to increase their sensitivity of chemotherapeutic agents. High levels of the IAP or NAIP proteins are selected in many cancers and are associated with poor prognosis, consisted that wild-type p53 suppresses transcription of the IAP or NAIP proteins and colon, are used to chemotherapeutic agents and mutations in p53 (it is genes). Transgenic animals are used for testing the effects of antisense colon colons.

CC cligonucleotides and for screening for the inhibitors.

CC cligonucleotides and for screening for the inhibitors.

CC cligonucleotides and for screening for the inhibitors.
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                                                                                                                                                                                                                                                                                                                          Inducing apoptosis in proliferative mammalian cells with inhibitor of IAP or NAIP polypeptide - also methods for prognosis based on presence of IAP and NAIP, specifically applied to cancers involving
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
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Best Local
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P-PSDB; W69295.
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13-FEB-1998; IB0781.
13-FEB-1997; US-800929.
(UYOT-) UNIV OTTAWA.
Baird S, Korneluk R, Liston P, Mackenzie AE, Pratt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO9835693-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Inhibitor of apoptosis protein; apoptosis enhancer; NAIP polypeptide; proliferative disease; IAP; therapy; cancer; human; HIAP-1 protein; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human HIAP-1
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54; Conservative
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4221. .6035
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Pred. No. 1.
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1;

Length 6669;

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Score

239;

DB ۳,

Length 32367;

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PT Turner's syndrome

PS Claim 19; Pages 51-67; 84pp; English.

CC This is the human SHOX gene sequence containing the PAR1 region. The gene CC region corresponding to short stature has been identified as a region of genes in this region have been identified as candidates for the short CC stature gene. These genes were designated SHOX (also referred to as SHOX93) or HOX93), pET92 and SHOT (SHOX-like homeobox gene on chromosome CC variations SHOXa and SHOXb. The specification provides sequences of SHOX (short stature homeobox-containing) genes SHOX ET92, SHOXA, SHOXb, SHOT CC sequences of the SHOX genes as shown in V35621 and protein CC and SHOT as shown W60573 to W60575. The novel genes are responsible for Treatment of short stature or other human growth genes short stature, e.g. CC treatment of short stature or other human growth disorders. The products can be used to develop agents for the CC can also be used for providing a mitogenic effect on cells, e.g. for the with disturbance in the bone calcium regulation.
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V35620
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with disturbance in the bone calcium regulation. Sequence 32367 BP; 7627 A; 8130 C; 8564
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16-JAN-1997; EP-100583
01-OCT-1996; US-027633
(RAPP/) RAFFOLD-HOERBRAND G.
RAO E, Rappold-hoerbrand G;
RPI; 98-271719/24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity
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W09814568-A1.
09-APR-1998.
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                                                                                                                                                                                                                                                                                                                                         New human growth genes - used and treatment of human growth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human SHOX (short stature homeobox containing gene) gene sequence Homeobox domain; human growth gene; growth regulation; growth defeturner's syndrome; short stature homeobox containing gene; SHOXa; SHOX; bone disease; osteoporosis; calcium regulation; short statu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               transcription factor A; ss.
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09-APR-1998.
29-SEP-1997; E05355.
16-JAN-1997; EP-100583.
01-OCT-1996; US-027633.
(RAPP/) RAPPOLD-HOERBRAND G
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Disclosure; Pages 37-45; 84pp; English.

This is a preliminary nucleotide sequence of the SHOX gene. The gene region corresponding to short stature has been identified as a region approximately 500 kb in the PARI region of the X and Y chromosomes. The genes in this region have been identified as candidates for the short
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Key
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                                                                such as short stature, e.g.
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HOX93; ss.
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Sequence: 15577 BP; 3692 A; 3875 C; 4196 G; 3629 T;
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                tgcagtgagcagagatcacaccactgcactctagcctgggtgacagagcaagactctgtc
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Pred. No. 1.2e
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RESULT
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pH15C insert
              "Aramalian cytokine synthesis inhibitory factors - capable of inhibiting synthesis of cytokine(s) associated with delayed type nypersensitivity and useful in treatment of e.g. leishmaniasis Disciosure; Fig. 4; 31pp; English
                                                                             28-JUN-1990; 307091
28-JUN-1989; US-372667.
20 LEC-1989; US-452951.
(5CHE ) SCHERING CORP.
MOSMICHN TR, MOOTE KW, BOND MW, Vleira
771; 31-009290/02.
                                                                                                                                                                                                                                                                                                                                                                       Q10207 standard; cDNA; Q10207;
    Disciosure;
The gene pr
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Best Local S
Matches 276
                                                                                                                                                                                      US5231012-A.
27-JUL-1993.
28-JUN-1989; 372667.
28-JUN-1989; US-372667.
20-DEC-1989; US-453951.
06-AUG-1999; US-46235.
20-JUL-1992; US-917806.
(SCHE) SCHERING CORP.
Genes and proteins encoding cytokine synthesis inhibitory factors - useful in treating diseases associated with cytokine imbalances, e.g. parasitic infections and auto-immune disorders Claim 1; Fig 4; 23pp; English.

A human T cell cDNA library was screened with probes based on the murine CSIF gene. Two clones carrying plasmids pH5C and pH15C were identified. (These two expression vectors are claimed). The CSIF polypeptide they encode inhibits synthesis of cytokines associated with delayed type hypersensitivity responses. CSIF (also called II-10) can be used to treat diseases associated with cytokine
                                                                                                                                                                  Bond
WPI;
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                                                                                                                                                                                                                                                                                                                                             mat_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                 myasthenia gravis; insulin-dependent
                                                                                                                                                                                                                                                                                                                                                                                                                             Human cytokine synthesis inhibitory factor clone pH15c. Mammalian cytokine synthesis inhibitory factor; CSIF; i IL-10; immune system imbalance; human T cell; Leischmar rheumatoid arthritis; systemic lupus erythematosus; thy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2030
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q46958 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25-JAN-1994
                                                                                                                                                                 MW, Moore KW,
93-249726/31.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9t99t9gcgcgtgcctgtaatcccagctactcgggaagctgaggcaggtgaattgtttga
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/product-
                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         entry)
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80.7%;
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Pred. No. 8e
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                                                                                                                                                                                Vieira
                                                                                                                                                                                                                                                                                                                                                                                                                n T cell; Leischmaniasis;
erythematosus; thyroiditis;
diabetes mellitus; ss.
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8e-49;
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C: This is the human SHOX gene sequence containing the PAR1 region. The gene corresponding to show that has been identified as a region of approximately 500 kb in the PAR1 region of the X and Y chromosomes. Three cidents in this region have been identified as candidates for the short contained the part of the X and Y chromosomes. Three cidents in this region have been identified as candidates for the short contained to as sequenced to as sequenced to a sequence of the SHOX gene has two separate splicing sites resulting in two contained to the SHOX and SHOX and SHOX peres as shown in V5611 and protein contained the show of the SHOX genes as shown in V5611 to V5561 and protein contained the shown with protein transcription factor SHOXA, SHOXD cond store of the SHOX genes as shown in V5610 to V5561 and protein contained the shown with protein transcription factor SHOXA, SHOXD cond SHOY as shown with SHOY5. The novel genes are responsible for human growth. Defects in the genes can cause short stature, e.g.

C: Turner's syndrome. The products can be used to develop agents for the products.
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Matches 276
                                                                                                                                                                                                                                                                                                                      Rao E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              07-SEP-1998 (first entry)
Human SHOX (short stature homeobox containing gene) ger
Homeobox domain; human growth gene; growth regulation;
turner's syndrome; short stature homeobox containing ge
SHOY; bone disease; osteoporosis; calcium regulation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1437
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2090
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                                                                                                                                                                                                                                                     Turner's syndrome
Claim 19; Pages 51-67;
                                                                                                                                                                                                                                                                                    New human growth genes and treatment of human
                                                                                                                                                                                                                                                                                                                                                                      16-JAN-1997;
01-OCT-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1910
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                                                                                                                                                                                                                                                                                                                     (RAPP/) RAPPOLD-HOERBRAND Rao E, Rappold-hoerbrand GWPI; 98-271719/24.
                                                                                                                                                                                                                                                                                                                                                                                                                        09-AFR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        transcription
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       V35620
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                                                                                                                                                                                                                                                                                                                                                                                                       29-SEP-1997;
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276; Conser
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nilarity 80.7%;
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      factor A;
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is, SLE, IDDM, myasthenia
; 463 A; 367 C;
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excessive production of
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growth
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                                                                                                                                                                                                                                                                                      develop products for
fects such as short st
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                                                                                                                                                                                                                                                                                                     the diagnosis
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can also be used for providing a mitogenic effect on a treatment of bone diseases such as osteoporosis and distinctbance in the bone calcium regulation.

Sequence 32367 BP; 7627 A; 8130 C; 8564 G;

diseases

involved ڣ

for the

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V35616/c
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Best Local S
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         09-APR-1998.
29-SEP-1997; E05355.
16-JAN-1997; EP-100583.
01-OCT-1996; US-027633.
01-OCT-1996; US-027633.
(RAPP) RAPPOLD-HOERBRAND G.
RAGO E, Rappold-hoerbrand G;
WPI; 98-271719/24.
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                                                                                                                                                                                                                                                                              SHOX; gene preliminary nucleotide sequence (HOX93).

Homeobox domain; human growth gene; growth regulation; growth defect; turner's syndrome; short stature homeobox containing gene; short stat SHOX; bone disease; osteoporosis; calcium regulation; HOX93; ss.
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                                                                                                                                                                                                                                                                      Homo sapiens
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                                                                            WO9814568-A1.
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3844. .
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11620.
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4326. .
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1498. .1807
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 genes - used
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    "pET92 region
    .4437

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Pred. No. 4.7e-48;
0; Mismatches 49
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                                                                                    IV (G108)
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Sequence 15577 BP; 3692 A; 3875 C; 4196 G; 3629 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This is a pruliminary nucleotide sequence of the SHOX gene. The gene region corresponding to short stature has been identified as a region of approximate; 500 kb in the PARI region of the X and Y chromosomes. Thre genes in the region have been identified as candidates for the short stature gene. These genes were designated SHOX (also referred to as SHOX) or ECX93), pET92 and SHOT (SHOX-like homeobox gene on chromosome three thre
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Disclosure; Pages 37-45; 84pp; Er
This is a proliminary nucleotide
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variations SHOXa and SHOXb. The specification provides sequences of
                                                                                                                                                                                                                                                TCACCTGAGGTCAGGAGTTCGAGACCAGCCTGGCCAACATGGTGAATCCCCGTCTTTACT
GCTGAGGCAGAGAATCGCTTGAACCCAGGAGGCGGAGGTTGCAGTGAGCCGAGATCGCA
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Similarity 84.4%;
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Pred. No. 3.4e-48;
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nucleic search, using sw model
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zt60d08 ah14e02

Insert Length: 816 Std Error: 0.00 Seq primer: -40UP from Gibco High quality sequence stop: 450. 1.673 1.673 /organism="Homo sapiens" /clone="IMAGE:2103714" /clone=lib="NCI_CGAP_Brn23" /tissue_type="glioblastoma (pooled)"	Contact: Robert Strausberg, Ph.D. Tel: (301) 496-1550 Email: Robert_Strausberg@nih.gov Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D. Ph.D. CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo, Ph.D. CDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Sequencing Cent Clone distribution: NCI-CGAP clone distribution information can found through the I.M.A.G.E. Consortium/LINL at: www-bio.llnl.gov/bbrp/image/image.html	ORGANISM Homo sapiens  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  Eutheria; Primates; Catarrhini; Hominidae; Homo.  1 (bases 1 to 673)  NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  NATITLE National Cancer Institute / National Institute of Neurological Disorders and Stroke, Brain Tumor Genome Anatomy Project (CGAP/BTGAP), Tumor Gene Index  JOURNAL Unpublished (1998)  COMMENT On Apr 7, 1998 this sequence version replaced gi:3035192.	RESULT 1 AI401218/c AI401218 673 bp mRNA EST 30-MAR-1999 LOCUS AI401218 673 bp mRNA EST 30-MAR-1999 DEFINITION tf60910.x1 NCI_CGAP_Brn23 Homo sapiens cDNA clone IMAGE:2103714 similar to SW:1131_HUMAN p78552 INTERLEUKIN-13 RECEPTOR ALPHA-1 CHAIN PRECURSOR; mRNA sequence. ACCESSION AI401218 NID 94244305 VERSJON AI401218.1 GI:4244305 KEYWORDS EST. SOURCE human.	11.2 448 48 AB155614 11.2 448 63 AIJ98370 11.2 448 63 AIJ98370 11.1 248 63 AWOO8384 11.1 448 44 AIZ275445 11.1 448 44 AIZ27764 11.1 448 45 AIJ342477 11.1 448 47 AIJ523044 11.1 445 41 AIJ17354 11.1 445 41 AIJ17354 11.1 446 63 AWOO6651 11.0 446 28 AA086290 10.9 446 62 AIB87698 10.9 447 62 AIB87698 10.9 448 43 AA086290 10.8 433 36 AA650015 10.8 433 36 AA650015 10.8 433 36 AA650015 10.8 433 36 AA650015 10.7 436 41 AIJ9262 10.8 437 42 AIJ9262 10.7 436 41 AA0974061 10.7 436 41 AA0974061 10.7 436 41 AA0974061 10.7 436 41 AA0974061 10.6 424 61 AIB89292 10.8 437 62 AIB97177 10.6 424 40 AA974061 10.6 424 61 AIB89292 10.5 420 45 AIJ67605 AIJ67605 AIJ677605 AIJ677605 AIJ677605 AIJ677605 AIJ677605 AIJ677605 AIJ677605 AIJ677605	23 449.2 11.2 454 51 AI744242 AI744242 24 448 11.2 448 42 AI088738 AI088738
Oy 1816 CLASCAGTC 1824	Qy 1636 a Db 193 A Qy 1696 g Db 133 G Db 133 G Db 1756 a Db 73 A	Db 37 Db 37 Db 31 Db 31 Db 157 Dy 157 Dy 25	Db 553 TCTGTAGTGCTGATAGAAACTTGAAGACAGCCTCTCAGTGATAGAGAGACTTATTTTT 4  Qy 1336 accttcactgtgaccttgagaagattcttcccatttgttatctgggaacttat 1  1	modified polylinker; Site_1: Not I; Site_2: Eco RI;  x	5.x

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Pred. No. 5.5e-107;
0; Mismatches 26;
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agccaagaaatgagtataggtaagaagcgcaattccacactctacataaccatgttactc
                                         ACACATAATGTTTTCTACGTCAAAGAGGCTAAATGTGAGAATCCAGAATNTGAGAGAAAT
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Unpublished (1997)
On Dec 20, 1995 th
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Emmert-Buck, M.D., Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 624)
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National Cancer Institute, Cancer Genome Anatomy
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                 Conservative
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Procurement: Christopher Moskaluk, M.D., Ph.D.,
                                                                                                                                                                                                                                                                                                                                                                               /note-*Organ: kidney; Vector: pT/T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: ECO RI; Plasmid DNA from the normalized library NCI_CGAP_Kid3 was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (cloneIDs 1322376-1323911, 1456007-1456775, and 1500552-1502855). Subtraction by Bento Soares and M. Fatima Bonaldo. "
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1) 496-1550
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/lab_host="DH10B"
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/map="9"
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                                                                                                                                                                                                                                                                                                         Seq primer:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert Strausbergenih.gov
Tissue Procurement: Elias Campo, M.D., Michael R.
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On May 18, 1995 this sequence version
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NCI-CGAP http://www.ocbi.nlm.nih.gov/ncicgap. National Cancer Institute, Cancer Genome Anatomy Pro
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ng30a07.sl NCI_CGAP_Co3
mRNA_sequence.
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Location/Qualifiers
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/tissue_type="colon"
/lab_host="DH10B"
/lab_host="DH10B"
/lab_host="T9T73D-Pac (Pharmacia) with a modified
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand
                                                                                                                                                      /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:936276"
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/sex="pooled"
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                            Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 627)
                                                                                                                                                                                           AI888989 627 bp mRNA EST 01-SEP-1999 wj16b01.x1 NCI_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2407953 3/Sinilar to SW:1131_HUWAN P78552 INTERLEUKIN-13 RECEPTOR ALPHA-1 CHAIN PRECURSOR ;, mRNA sequence.
   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anat
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                                                                                                                                           GI:5594153
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aactaggggacaaagcaaaaagtgatgatagtggtggagttaatcttatcaagagttgtg
                                                     aaaaggctcaagattattatattccctccaattcctgatcctggcaagatttttaaagaa 1194
                                                                                                                                                                                               atttgtratctgggaacttattaaatggaaactgcaactactgcaccatttaaaaacagg
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Tel: (301) 496-1550
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                                                                                                                                                                                                                                                                                                                                                                                                This is the 5' sequence of the clone insert Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DRT2); Email s.wiemannddAfz- heidelberg.de; sequenced by Olagen within the cDNA sequencing consortium of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 673)
Duesterhoeft,A., Lauber,J., Mewes,H.W., Gassenhuber,
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This clone is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerwe
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
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/clone_lib="564 (synonym:
/tissue_type="brain"
/dev_stage="fetal"
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/db_xref-"taxon:9606"
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                                                                                                   Contact: Robert Strausberg, Ph.D Tel: (301) 496-1550
Email Robert_Strausberg@nih.gov
www-bio.llnl.gov/bbrp/image/image.html
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           found through the I.M.A.G.E.
                                                                            Emmert-Buck, M.D., Ph.D.
                                                                                        Tissue Procurement:
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                       CDNA Library Preparation: M. Bento Soares, Ph.D. CDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Clone distribution: NCT-CGAP clone distribution
                                                                                                                                                                                                                                                                                                GI:5435870
                                                                                        Christopher Moskaluk, M.D.,
           Consortium/LLNL at:
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Unpublished (1997)
On Tur. 5, 1998 this sequence version
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1 (bases 1 to 571)
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National Cancer Institute. Cancer Genome Anatomy
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Location/Qualifiers
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/tissue_type="2 pooled tumo:
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/clone="IMAGE:2404697"
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/db_xref="taxon:9606"
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Pred. No. 3.3e-95;
D; Mismatches 0;
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RESULT NA411323

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jos Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin, J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F., Theising, B., White, Y., Wylie, T., Waterston, R. and Wilson, R. Washu-Merck EST Project 1997
Unpublished (1997)
On Sep 12, 1996 this sequence version replaced gi:1406976.
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INAGE:755037 5', mRNA sequence
AA411323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This clone is available royalty-free through LLNL; MAGE Consortium (info@image.llnl.gov) for further: Seq primer: -28m13 rev2 ET from Amersham High quality sequence stop: 500.
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Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutherja; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1:to 533)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             double-stranded cDNA was size selected, ligated to Eco adapters (Pharmacia), digested with Not I and cloned in the Not I and Eco RI sites of a modified pT7T3 vector (Pharmacia). Library constructed by Bento Soares and M.Fatima Bonaldo. "
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/db_xref="taxon:9606"
/clone="IMAGE:755037"
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Unpublished (1997)
On Jun 5, 1998 this
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wm17d11.x1 NCI_CGAP_Ut4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy
                                                                                                                                                                                                                                                                                     www-bio.llnl.gov/bbrp/image/image.html
                                                                                                                                                                                                                                                                                                CDNA Library Preparation: Life Technologies, Inc. CDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome S Clone distribution: NCI-CGAP clone distribution i found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                          Email: Robert_Strausberg@nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Robert Strausberg,
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               179
                                                                                                                                                                                                                                        quality sequence stop: 408.
                                                                                                                                                                                                                                                                                                                                                                                                                      (301) 496-1550
               þ
                            /note-"Organ: uterus; Vector: pCMV-SPORT6; Site_1: SalI; Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.48 kb. Life Technologies catalog #: 11542-016"
                                                                                                     /tissue_type="serous papillary carcinoma, high
pooled tumors"
                                                                                                                                                                /db_xref="taxon:9606"
/map="21q; 56cM"
                                                                                                                                                /clone="
                                                                                                                                  /clone_lib="NCI_CGAP_Ut4"
                                                                                                                                                                                          organism="Homo sapiens"
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                                                                                     lab_host="DH10B"
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A clone IMAGE:2436213 3',
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Query Match

13.0%;

Score

521;

DB 62;

Length 521;

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RESULT 9
AA669035/c
LOCUS
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                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalis Butheria; Primates; Catarrhini; Hominidae; Homo.

1. (bases 1 to 507)

Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost Krizman,D., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B., White,Y., Wylie,T., Waterston,R. and Wilson,R. Washu-NCI human EST Project
Unpublished (1997)
On Nov 6, 1997 this sequence version replaced gi:932221.
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Seq primer: -40ml3 fwd. ET from Amersham High quality sequence stop: 455.
                                                                                                                                                                                                                                                                                                                                                                                                                            A2669035 507 bp
ab88g12.s1 Stratagene
IMAGE:854086 3', mRNA
                                                                                        Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                      Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St.
                                                                                                                                                    Contact: Wilson RK
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                                                                          Email: est@watson.wustl.edu
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                                                                                                                                                                                                                                                  th82f08.x1 Soares_NhHMPu_S1 Homo sapiens
3', mRNA sequence.
A1436787
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap
                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 504)
                                                                                                              Homo sapiens
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//lab_host="50ft cells (kanamycin resistant)"
//lab_host="50ft cells (kanamycin resistant)"
//note="forgan: lung; Vector: pBluescript SK:; Site_1:
//note="forgan: lung; Vector: pBluescript SK: Primer:
//note="forgan: lung; Vector: pBluescript Size: 10 kb;
//note="forgan: lung; Vector: 5"
//note="forgan: lun
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/clone_lib="Stratagene lung
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/db_xref="taxon:9606"
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ttggtagtcttcaaccagggattgtttctgttttaaccttcttataggaaagcttgagtaaa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACATTGATGCTGACAGTCATGCAGTCTGGGAGTGGGGAAGTGATCTTTTGTTCCCATCCT
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                                                                                                                                                                         cagttaagtttttcccttcatctgggcactgaagggatatgtgaaacaatgttaacattt
                                                                                                                                                                                                                                                                                                                                           ttttttcctaacatacctaagcaaacccagtgtcaggatggtaattcttattctttcgtt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | tcccatcccctgtgggaaattagtaggctcatttactgttttaggtctagcctatgtgga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cttcttttagcagtaaaatagctgagggaaaagggaagggaaaaggaagttatgggaatac 367.
                                                                                                                                                                                                                                                                                               TTTTTTCCTAACATACCTAAGCAAACCCAGTGTCAGGATGGTAATTCTTATTCTTTCGTT 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TCCCATCCCCTGTGGGAAATTAGTAGGCCCATTTACTGTTTTAGGTCTAGCCTATGTGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CTGTGGTGGTGTGATCCCTAGGTCTTGGGAGCTCTTGGAGGTGTCTGTATCAGTGGATT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    On May 18, 1998 this sequence version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tumor Gene Index
Unpublished (1997)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       High quality sequence stop: 465.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Site_2: Eco RI; Equal amounts of plasmid DNA from three normalized libraries (melanocyte 2NbHM, pregnant uterus NbHPU, and fetal heart NbHH19W) were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of I.M.A.G.E. clones 260232-265223, 340488-345479, and 484488-489479."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             pregnant uterus"
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/db_xref="taxon:9606"
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/tissue_type="Pooled human me]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12.6%; Score 504; DB 46; 100.0%; Pred. No. 4.5e-84; tive 0; Mismatches 0;
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gaggcgggcggatcactcgaggtcaggagttccagaccagcctgaccaaaatggtgaaac 1934
                                                            TTTAACAGTCTGGGCTGGGTCCGGTGGCTCACGCCTGTAATCCCCAGCAATTTGGGAGTCC 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This clone is available royalty-free through LLNL; contact the IMAGE Consortium (infedimage.llnl.gov) for further information. This read is a RESEQUENCE of a previously sequenced human clone original clone citation: see original entry for original citatic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCI/NIDR-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute / National Institute of Dental Research,
Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
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ah14e02.y5 Gessler Wilms
IMAGE:1156634 5' similar
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                         /note="vector: pspOrT1; Site_1: SalI; Site_2: NotI; RNA
was prepared from a pool of 6 anonymous Wilms' tumor RNAs.
RNA was prepared by acid-phenol, followed by one round of
oligo dT selection. cDNA library preparation was with
the BRL/Life Tech. Superscript plasmid system. An
oligo-dT NotI primer for first strand synthesis generated
gcggccgcc(t)n at the 3' end of the clones. A 5' SalI
adaptor was used with sequence 5'-gtcgaccacggctccg-3'.
Resulting cDNAs were size selected (average size 2 kb),
NotI digested, and ligated into NotI/SalI-cut pspORT1.
Library was constructed by Dr. Manfred Gessler."

46 a 118 c 124 g 111 t 2 others
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/sex="pooled (6)"
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0; Mismatches 2;
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1 (bases 1 to
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                                                                                                                                                                                                                                                                                                                                      Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Wilson washington University School of Medicine Washington Transcriptor Box 8501, St. Louis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Insert Length: 788 Std Error: 0.00
Seq primer: -41m13 fwd. ET from Amersh
High quality sequence.stop: 406.
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Fax: 314 286 1810
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                        /clone_lib="Soares_testis_NHT"
                                                      /db_xref="taxon:9606"
/clone="IMAGE:726735"
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             Eukaryota; Metazoa; Chordata; Craniata; Verte
Eutheria; Primates; Catarrhin; Hominidae; Ho
1 (bases 1 to 478)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer
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//lab_host="NH10B"
//note="Vector: pTT3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cD was prepared from mRNA obtained from Clontech Laboratories, Inc., and primed with a Not I - oligo(dT) primer [5'
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Pred. No. 3.9e-80;
0; Mismatches 2
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Genome Anatomy
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Pest Local Similarity 100.0%;

Matches 477; Conservative
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                tgtttaacttcttataggaaagcttgagtaaaataaatattgtctttttgtatgtca 3996
                                                       CTGAAGGGATATGTGAAACAATGTTAACATTTTTGGTAGTCTTCAACCAGGGATTGTTTC
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TGTTTAACTTCTTATAGGAAAGCTTGAGTAAAATAAATATTGTCTTTTTGTATGTCA
                                                                                                               AGTGTCAGGATGGTAATTCTTATTCTTTCGTTCAGTTAAGTTTTTCCCTTCATCTGGGCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tumor Gene Index
Unpublished (1997)
On Jan 19, 1998 th
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: Robert_Strausberg@nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Robert Strausberg, Ph.D
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/db_xref="taxon:9606"
/clone="IMAGE:1739756"
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3551 aacattgatgctgacagtcatgcagtctgggagtggggaagtgatcttttgttcccatcc
                                                                                                                                 3492 catttttactgttatcctattta-gatggccatgaagaggatgctgtgaaattcccaaca 3550
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                                                                                                      CATTTTTACTGTTACCCTATTAAGGATGNCCATGAAGAGGATGCTGTGAAATTCCCAACA 448
                                                                                                                                                                                                                                       500;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IMAGE Consortium (info@image.llnl.gov)
Insert Length: 617 Std Error: 0.00
Seq primer: -40M13 fwd. from Amersham
High quality sequence stop: 424.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: estewatson.wustl.edu
Email: estewatson.wustl.edu
This clone is available royalty-free through LLNL; contact the
This clone is available royalty-free through LLNL; contact the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis,
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Wilson RK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hillier, L., Lennon, G., Becker, M., Bonaldo, M.F., Chiapelli, B., Chissoe, S., Dietrich, N., DuBuque, T., Favello, A., Gish, W., Hawkins, M., Hultman, M., Kucaba, T., Lacy, M., Le, M., Le, N., Le, M., Le, 
                                                                                                                                                                                                                                    Similarity 98.0
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                                                                                                                                                                                                                                                                          Contact: Wilson RK
Washington University Scho
4444 Forest Park Parkway,
Tel: 314 286 1800
Fax: 314 286 1810
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1 (bases 1 to 485)

Hillier, L. Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost, S. Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin, J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F., Theising, B., White, Y., Wylie, T., Waterston, R. and Wilson, R. washu-Merck EST Project 1997

Depolitished (1997)
                                                                                                                                                               Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL;
IMAGE Consortium (info@image.llnl.gov) for further i
Seq primer: -4lml3 fwd. ET from Amersham
High quality sequence stop: 467.
Location/Qualifiers
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                                                                                          /organism="Homo sapiens"
/db_xref="taxon:9605"
/clone="IMAGE:755037"
/tissue_type="ovarian tumor"
/lab_host="DH10B (ampicillin resistant)"
/ncte="Organ: ovary; Vector: pT7T3D (Pha
                                                          /sex="Female"
                                                                           /clone_lib="Soares ovary
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CACAAAGAACATGTAGAAAACAAAATGGATAAAATCTGATATGTATTGTTTGGGA 11
                    cacaaagaacatgtagaaaacaaaatggataaaatctgatatgtattgtttggga 1779
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                                                                                                                                                                                                                                                                                                                                                                                          TAAAAAACAGGCAGCTCATAAGAGCCACAGGTCTTTATGTTGAGTCGCGCACCGAAAAAACT 306
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M.Fatima Bonaldo. "
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Search completed: January 20, 2000, 05:25:49 Job time: 6362 sec

GenCore version 4.5 Copyright (c) 1993 - 1998 Compugen Ltd.

OM protein - protein search, using sw model

January 19, 2000, 17:31:45; Search time 34.07 Seconds (without alignments) 264.183 Million cell updates/sec

W35295

W35295; 27-MAR-1996

W35295 stardard; Protein; 380 AA.

Muman IL-13 binding

chain of the IL-13 receptor

Perfect score: US-09-077-817-2

sequence: 1 MAFVCLAIGCLYTFLISTTF......LLLRKPNTYPKMIPEFFCDT 380

Searched: 188963 seqs, 23686106 residues Scoring table:

BLOSUM62

Database : A\_Geneseq\_36:\*

Word size :

0

Number of hits that pass the threshold : 188963

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

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Conservative

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Mismatches

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R78616	R78610	R20932	W56257	R92529	R78608
Expression vector	Expression vector	Sequence of beta-c	Interleukin-13 bin	Fas sequence from	Murine IL-3 recept

## ALIGNMENTS

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The present sequence represents the human interleukin-13 (IL-13) binding chain of the interleukin-13 receptor, designated IL-13bc. IL-13bc acts a mediator of the known biological activities of IL-13. Recombinant IL-13bc proteins, and antibodies raised against them, are used to inhibit the binding of IL-13 to its receptor. They are particularly used to treat IgE-mediated conditions, e.g. allergy, asthma and immune complex disorders, especially lupus, nephritis, thyroiditis and drawe's disease. They are also used to treat immune deficiency (particularly in haematopoietic progenitor cells), cancer etc., and to increase macrophage activation, e.g. in vaccingtion. To potentiate IL-13 activity, a protein with such activity is combined with IL-13bc and the mixture applied, in vivo, to activity is combined with IL-13bc and the mixture applied, in vivo, to cell expressing at least one chain of the IL-13 receptor other than IL-13bc. IL-13bc can also be used in diagnosis to detect antibodies which may be useful for treating some tumours.
Query Match
3675 Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New nucleic acid encoding interleukin-13 receptor binding chain and transformed cells - proteins, antibodies and inhibitors, for treating immunoglobulin E-mediated diseases, e.g. Graves disease,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gollins M, Donaldson D, Fitz L, Neben T, Whitters Wood C; Will: 97-448632/41.
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/note= "putative"
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       100.0%; Score 2104; DB 1; 100.0%; Pred. No. 8.1e-194;
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                      PT New nucleic acid encoding testis-specific cytokine receptor - useful PT New nucleic acid encoding testis-specific cytokine receptor - useful PT male contraceptives or for infertility treatment Claim 2; Page 47-48; 79pp; English.

CC This sequence represents a novel ligand-binding receptor, Zcytor2, CC which shares homology with cytokine receptors and was isolated from human CC placental polya+ RNA. The resulting polyapeptide is a receptor for CC cytokines (particularly interleukin-13) and is expressed on the surface CC cytokines (particularly interleukin-13) and is expressed on the surface CC cytokines (particularly interleukin-13) and is expressed on the surface CC differentiation of such cells in cultures and may also be used to treat infertility. Antagonists of this receptor may be used to characterise CC ligand-receptor interactions and as male-specific contraceptives. By CC ligand-receptor can also be used to modulate immune function, e.g. in CC alienty the action of II-13, receptor antagonists and ligand-binding CC this receptor can also be used to modulate immune function, e.g. in CC contraceptives. By contraceptive can be used to disease such as cancer), for labelling cells that express the receptor, and the receptor, as antagonists.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human zcytor2 cytokine receptor protein.
Cytokine receptor; ligand binding; testicular cell; spermatogenesis;
infertility; antagonist; contraceptive; diagnostic; therapeutic.
                                                                                                                                                                                                                                                                                                                                                 N-PSDB; T96782.
Sequence
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12-MAR-1997; U04043
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17-DEC-1997. 303815:
04-UUN-1997; 303815:
x 12-UUN-1996; US-017343. x 12-UUN-1996;
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This protein comprises a novel human cytokine/peptide hormone receptors/designated HR-1 receptor. The amino acid sequence was deduced from a cDNA clone (see v04075) isolated from a human testis cDNA library. It shows 27% amino acid identity and 52% similarity with the human interleukin-5 receptor. Also claimed are polynucleotides encoding HR-1 receptor, vector and host cells, an agonist to the polypeptide, antibody against the polypeptide, an antagonist that inhibits the activity of the polypeptide, a process for diagnosing a disease, or a susceptibility to disease, related to expression of HR-1 receptor, and a method for identifying compounds that activate or inhibit the HR-1 receptor. HR-1
                                                                                                                                                                                                                                                                                                                                    N-PSDB; v04075.
Human cytokine/peptide hormone receptor, HR-1 receptor - useful to
increase resistance to infections in individuals with trauma and/or
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HR-1 receptor; cytokine receptor; peptide hormone receptor; human;
infection; burn; trauma; asthma; allergy; AIDS; aplastic anaemia;
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                                                                                                                                                                                                                                                                                                     Claim 13; Page·27-28; 34pp; English.
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WPI; 98-034974/0
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Pred. No. 8.1e-194;
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Best Local :
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Homo saplens HR-1 receptor; AIDS; acquired immune deficiency; Cytokine; hormone receptor; AIDS; acquired immune deficiency; syndrome; aplastic ansemia; neutropaenia; cancer treatment; syndrome; aplastic ansemia; neutropaenia; HR-1 receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              receptor protein and polynucleotides can be used for research, biological, diagnosis and (gene) therapy applications, e.g. to increase resistance to infections in individuals with trauma and/or burns, and to prevent, ameliorate, treat, diagnose and/or determine predisposition to asthma, allergic disorders or disorders of haematopoiesis induced by AIDS, aplastic anaemia, congenital or cyclic neutropaenia or as a consequence of cytotoxic therapy of cancer, lymphoma, leukaemia and/or bone marrow transplantation. Sequence 380 AA;
DNA encoding human cytokine-peptide hormone receptor treating preventing or diagnosing, e.g. lowered resisting infection, asthma, allergy, or haematopoietic disease Claim 15; Fig 1; 75pp; English.

The sequence is that of the human cytokine/peptide hormone is the control of the sequence is that of the human cytokine/peptide hormone is the cytokine/peptide ho
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09-UU-1996; U11459

12-UUN-1996; WO-U10262

12-UUN-1996; US-017843

(HUMA-) HUMAN GENOME SCI INC.

(SMIK.) SMITHKLINE BEECHAM CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    W33603 standard; Protein; W33603;
                                                                                                                                         N-PSDB; V02295
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Pred. No. 8.1e-194;
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                                                                                                                                                  SMET ) SANOFI SA.

SMET ) SANOFI SA.

SAPUT D, FETTRATA P, Laurent P,

APIT 97-319773/29,

APIT 97-319773/29,

MRS826, T88464.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (HR-1 receptor). This, or it's activators or agonists, can be used to treat, prevent or diagnose predisposition to lowered resistance to infection; asthma, allergic or haematopoietic disorders, e.g. where indured by acquired immune deficiency syndrome (AIDS), aplastic anaemia, neutrop, ania or cytotoxic treatments for cancer. Antagonists of the receptor, e.g. antibodies or fragments of it may be used to treat conditions associated with overexpression of the HR-1 receptor, e.g. hose listed above. Antibodies may also be used to assay levels of HR-1 receptor; overexpression of which may be diagnostic of tumours, by usual lumminoassays; to isolate and identify HR-1 receptor expressing cells; or finity purification of the HR-1 receptor.
invention relates to new purified peptides comprising 380 or 427 amino acid sequences, which are receptors for interleukin-13 (IL-13); the 380 and 427 aa proteins are designated IL-13R beta and alpha respectively. The IL-13R beta has high affinity for IL-13 while IL-13R alpha has low affinity, but acquirs high affirity when associated with the IL-4
                                                   This sequence represents interleukin-13 (IL-13) beta receptor. The invention relates to new purified peptides comprising 380 or 427 ami acid sequences, which are receptors for interleukin-13 (IL-13); the
                                                                                                                                     acids,
                                                                                                                                                                                                                                                                                    Homo sapiens. WO9720976-A1.
                                                                                                                                                                                                                                    12-00N-1997.
07-NOV-1996; F01756.
%6-DFC-1995; FR-014424.
                                                                                                                                                                                                                                                                                                                                         Human interleukin-13 beta
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                                                                                                    laim 1; Figure 2a; 83pp; French
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                                                                                                                                   purified human interleukin-13 receptors %, useful for diagnosis and treatment of
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3.1e-194;
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    and related inflammation,

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Best Local S
Matches 380
                 18-DEC-1997.
12-JUN-1995; U10262.
12-JUN-1996; WO-U10262.
(HUMA-) HUMAN GENOME SCI INC.
(SMIK ) SMITHKLINE BEECHAM COR
Appelbaum ER, Hu J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      receptor. Nuc
diagnostic pr
such as loss
Appelbaum ER, Hu w
WPI; 98-052308/05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HR-1 receptor;
haematopoietic
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                                                                                                                                                                                                                                       W09747741-A1.
                                                                                                                                                                                                                                                                                                              Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human HR-1 receptor
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22. .380
/label= Mat_protein
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Pred. No. 8.1e-194;
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This protein comprises a novel human cytokine/peptide hormone receptor, designated the HR-1 receptor, that shows 27% identity and 52% similarity to the interleukin-5 receptor. Its amino acid sequence was deduced from a CDNA clone (see VQ4131) obtained from a channel from the sepressed in claimed host cells, and used in a claimed method for identifying compounds which bind to, and activate or inhibit, it. HR-1 receptor activators and agonists can be used to treat, prevent or diagnose predisposition to lowered resistance to infection, asthma, allergic or haematopoletic disorders, e.g. where induced by AIDS, aplastic mamemia, neutropaenia or cytotoxic treatments for cancer. HR-1 antagonists, e.g. antibodies or HR-1 receptor fragments, can be used to treat conditions associated with HR-1 receptor levels, since overexpression may be diagnostic of tumours.
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Best Local
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18-SEP-1997
12-MAR-1997; U04043.
13-MAR-1996; US-013345.
(ZYMO) ZYMOGENETICS INC
Baumgartner JW, Farrah T
                                                                                                                 Human Zcytor2 cytokine receptor protein. Cytokine receptor; 'ligand binding; testicular cell; infertility; antagonist; contraceptive; diagnostic;
                                                                                    Homo sapiens.
WO9733913-A1.
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30-MAR-1998
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Pred. No. 8 1e-194;
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PT New nucleac acid encoding testis-specific cytokine receptor - useful PT for identification of ligands or antagonists, potentially for use as property for intertility treatment contraceptives or for intertility treatment contraceptor. Zeytor2, which contraces because represents a novel ligand-binding receptor. Zeytor2, which contraces because contraction convertible in contractions and was isolated from a human contraction contraction contraction. The resulting polypeptide is a receptor for cytokines (particularly intersleukin-13) and is expressed on the surface of testicular cells, probably being involved in spermatogenesis. It can contract to differentiation of such cells in cultures and may also be used to treat contracterise contractions and as male-specific contraceptives. By blocking the action of II-13, receptor antagonists and ligand-binding contraction; e.g. in contraction can also be used to modulate immune function, e.g. in contraction and as males of determine circulating levels of contraction and as antagonist. The determine circulating levels of contraction and contraction and and also to isolate and purify ligands. Antibodies can be used to cand they are contracted to a santagonist.
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Best Local Similarity
Matches 377; Conserv
                                                                                                                                    Celebus macaque Zcytor2 protein.
Cytokine receptor; ligand binding; test
infertility; antagonist; contraceptive;
W09733913-A1.
18-SEP-1997.
12-MAR-1997; U04043
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99.2%;
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No. 2.5e-191;
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tive; diagnostic;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local S
Matches 343
Homo sapiens.
WO9810539-A1.
19-MAP-1993.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New nucluic acid encoding testis-specific cytokine receptor - usef for identification of ligands or antagonists, potentially for use male contraceptives or for infertility treatment Example 4; Page 56-57; 79pp; English.
                                                           Construct containing mature interleukin-13 binding "herapeutic; IL-3 mediated condition; allergy; ast
                                                                                          W56260 standard; Protein; W56250; first entry)
                                              autoimmune disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CHara
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    express the receptor, and therapeutically as antagonist. Sequence 372 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13-MAR-1996: US-013345.
(ZYMO) ZYM SENETICS INC.
Baumgartter JW, Farrah TN
                                                                                                                                                                                                         361
                                                                                                                                                                                                                                                                                                   301
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                                                                                                                                                                                                                                                                  TRQI.CF: VRSKVNIYCSDDGIWSFWSDKQCWEGEDLSKKTLLRFWLPFGFILILVIFVTG
                                                                                                                                                                                                                                                                                                                                  PVCLTCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SSWAETTYWISPQGIPETKVQDMDCVYYNWQYLLCSWKPGIGVLLDTNYNLFYWYEGLDH 180
                                                                                                                                                                                                         LLLCKRDSYPKM
                                                                                                                                                                                                                                     LLLRKPNTYPKM
                                                                                                                                                                                                                                                                                                                                                               PVYLOTTEESSCEIKLKWSIPLGPIPARCEDYEIEIREDDTTLVTATVENETYTLKTTNE
                                                                                                                                                                                                                                                                                                                                                                                               ALQCVDYIKVDGQNIGCRFFYLESSDYKDFYICVNGSSETKPIRSSYFTFQLQNIVKPLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                            SSWAEATYWISPQGIPETKVQDMDCVYYNWQYLLCSWKPGIGVLLDTNYNLFYWYEGLDR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NFKECTVEYELKYRNIGSETWTTIITKNLHYKDGFDLNKGIEAKIHTLLPWQCTNGSEVQ
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                                                                                                                                                                                                                                     372
                                               antibody;
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Pred. No. 9.2e-170;
7; Mismatches 22;
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RESULT 10
W56261
ID W56261
AC W56261
DT 16-SEP
DE Mature
KW Therap
KW HOMOO'S
FN W09810
OP 19-MARA
PF 10-SEP
PA (AMRA-
PI Hilton
DR WPI;
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PI HILTON
DR WPI HILTON
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Best Loc
Matches
                                                                                                          10-SEP-1997; AU0591.
27-FEB-1997; AU-005374.
10-SEP-1996; AU-002262.
(AMRA-) AMRAD OPERATIONS PHilton DJ, Nicola NA, Simp WPI: 98-207062/18.
N-PSDB; V22702.
New isolated interleukin-13 binding products for therapy e.g. for allers for diagnosis or detection bisclosure; Page 55-56; 69pp; Englis The II-13 binding protein and relate
                                                                                                                                                                                                                                                                            Homo sapiens.
WO9810638-Al.
                                                                                                                                                                                                                                                                                                                                                               Mature interleukin-13 bind
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New isolated interleukin-13 binding protein - used to develop products for therapy e.g. for allergic conditions such as asthma (for diagnosis or detection)

Example 14; Page 52-53; 69pp; English.

The IL-13 binding protein and related therapeutic molecules can be in the antagonism of at least one IL-13 activity. They can be used treating IL-13 mediated conditions such as certain allergic conditions such as asthma or to inactivate locally administered IL-13 after treatment. The products can also be used as diagnostic agents, edetecting autoimmune diseases. The antibodies can also be used for immunotherapy and may also be used as a diagnostic tool.
                                                                                                                                                                                                                                                                                                                       autoimmune disease;
                                                                                                                                                                                                                                                                                                                                           Therapeutic;
                                                                                                                                                                                                                                                                                                                                                                                                                       W56261 standard;
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27-FEB-1997; AU-005374.
10-SEP-1996; AU-002262.
(AMRA-) AMRAD OPERATIONS PTY I
Hilton DJ, Nicola NA, Simpson
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N-PSDB; V22701.
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Local Similarity 100.0%;
les 315; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     leukin-13 binding protein.
IL-3 mediated condition; allergy; asthma; diagnosis;
isease; antibody; immunotherapy.
                                                                                                                                                                                                                                                                                                                                                                                                                       Protein;
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28-FEB-1997; 1
01-MAR-1996; 1
                                                                                                                                                    (GEMY )
                               New nucleic acid encoding transformed cells - protei
                                                                                 N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Murine IL-13 binding chain of the IL-13 receptor. Interleukin-13; IL-13; interleukin-13 receptor binding chain; IL-13bc; mediator; IL-13 receptor binding inhibition; IgB-mediated condition;
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Local Similarity
thes 315; Conserv
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97-448632/41.
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                                                                                 T75213
                                                                                                                                                  M, Donaldson D,
                                                                                                                                                                       GENETICS INST 1
           immunoglobulin
                                                                                                                                                                                                                     U03124
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                                                                                                                                                                                                                                                                                                         /label=
.357. ~~
                                                                                                                                                                                                                                                                                           /label-
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/note= "putative"
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                                                                                                                                                                                                                                                                                                                                                                                 Label=
                                   proteins,
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                                                                                                                                               INC.
D, Fitz
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       ng interleukin-13 receptor binding chain teins, antibodies and inhibitors, for B-mediated diseases, e.g. Graves disease
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                                                                                                                                                                                                                                                                                                                                 transmembrane_domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      complex disorder.
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Pred. No. 2.8e-160;
0; Mismatches 0;
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                                                                                                                                           Whitters
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  chain of the interleukin-13 receptor, designated IL-13bc IL-13bc acts a mediator of the known biological activities of IL-13. Recombinant IL-13bc proteins, and antibodies raised against them, are used to inhibit the binding of IL-13 to its receptor. They are particularly used to treat IgE-mediated conditions, e.g. allergy, asthma and immune complex disorders, especially lupus, nephiritis, thyroiditis and Grave's disease. They are also used to treat immune deficiency (particularly in haematopoietic progenitor cells), cancer etc., and to increase macrophage activation, e.g. in vaccination. To potentiate IL-13 activity, a protein with such activity is combined with IL-13bc and the mixture applied, in vivo, to a cell expression at least one chain of the IL-13 receptor other than IL-13bc. IL-13bc can also be used in diagnosis to detect expression of IL-13, its receptor or binding chain, and to raise specific antibodies which may be useful for treating some tumours.
                                                                                                                                                                                                         Interleukin-13 binding protein N-terminal ORF Therapeutic; IL-3 mediated condition; allergy; autoimmune disease; antibody; immunotherapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 11; Pages 30-31; 49pp;
The present sequence represent chain of the interleukin-13
             Misc_difference
                                                                                                                                                                                                                                                                               W56252 standard; Protein; 157 W56252;
                                                                                                                              Misc_difference
                                                                                                                                                                                              Homo
                                                                                Misc_difference
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MAFYCLAIGCLYTFLISTTFGCTSSSDTEIKVNPPQDFEIVDPGYLGYLYLQWQPPLSLD
                                                                                                                                                                                                                                                                                                                                                                              LIVEKEEPEPTL 365
                                                                                                                                                                                                                                                                                                                                                                                                             LLLRKPNTYPKM 372
                                                                                                                                                                                                                                                                                                                                                                                                                                            SEDICFFVRCKVNIYCADDGIWSEWSEEECWEGYTGPDSKII-FIVPVCLFFIFLLLLLC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PVYLTFTRESSCEIKLKWSIPLGPIPARCFDYEIEIREDDTTLVTATVENETYTLKTINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KFKGCTLEYELKYRNVDSDSWKTIITRNLIYKDGFDLNKGIEGKIRTHLSEHCTNGSEVQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ages 30-31; 49pp; English.

sequence represents the murine interleukin-13 (IL-13) binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                              (first entry)
                                                                              /note= "Encoded by
                                                                                                                                     /note= "Stop codon"
                                                                                                                                                                            Location/Qualifiers
/label= Unknown
                                                                                                              /label- Unknown
                                note-
                                                             note-
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                                "Putative signal sequence"
                                                             "Stop codon"
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                                                                                                                                                                                                                           allergy;
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Fest Local
Chaim 21; Page 42-44; 65pp; English.

The inventors claim: an isolated cDNA sequence encoding murine (secretory) interleukin-5 (IL-5) receptor, which is synthesised from murine early P cell mRNA; an isolated murine (secretory) IL-5 receptor: an isolated cDNA sequence encoding human (secretory) IL-5 receptor; which is synthesised from mRNA of human peripheral blood eosinophil; and an isolated human; (secretory) IL-5 receptor. Also claimed are u COS monkey cell transfected with a recombinant vector contg. the DNA; secretory human IL-5 lacking a cytoplasmic and a transmembrane region; and an expression vector.

Sequence 396 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New isolated interleukin-13 binding protein - used to devalop products for therapy e.g. for allergic conditions such as asthma or for diagnosis or detection.

Claim 7; Page 44; 69pp; English.

The IL-13 binding protein and related therapeutic molecules can be used in the antagenism of at least one IL-13 activity. They can be used for treating IL-13 mediated conditions such as certain allergic conditions such as asthma or to inactivate locally administered IL-13 after IL-13 such as asthma or to inactivate locally administered IL-13 after IL-13
                                                                                                                                                                                                                                                           11-5EP-1991; 308309.
17-5EP-1990; JP-240638.
(TAKA,') TAKATSU K.
Takatsu K. Tominaga A. Takagi S. Murata
WPI, 92-090329/12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                treatment. The products can also be used as diagnostic agents, e.g. detecting arroimmune diseases. The antibodies can also be used for immunotherapy and may also be used as a diagnostic tool. Sequence .57 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Misc_difference
                                                                                                                                                                                                                     Human and murine interleukin-5 receptor and DNA encoding for treatment of auto-immune and eosinophilia conditions
                                                                                                                                                                                                                                                                                                                                                                                                                 sequence of human interleukin S receptor with signal peptide (from a patient of eosinophilia).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R22216 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hilton DJ, Nicola
WPI; 98-207062/18.
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Hilton DJ, Nicola NA, Simpson RJ,
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27-FEB-1997;
                                                                                                                                                                                                 involving IL-5
                                                                                                                                                                                                                                                                                                                                                      7-MAR-1992.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 HFKEC:VEYELKYRNIGSETWK--TIITKNLHYKDGFDLNKG-IEAKI-HTLLP 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    43 MAFVCIAIGCLYTFLISTTFGCTSSSDTEIKVNPPQDFEIVDPGYLGYLYLQWQPPLSLD 102
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77.2%;
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Pred. No. 2.4e-36;
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Best Local :

Similarity

14.8%;

Score 311.5; DB 1; Pred. No. 6.2e-22;

Length 396;

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Disclosure; Page 49; 65pp; English.
Disclosure; Page 49; 65pp; English.
The inventors claim: an isolated cDNA sequence encoding murine (secretory) interleukin-5 (II-5) receptor, which is synthesised from murine early B cell mRNA; an isolated murine (secretory) II-5 receptor; an isolated cDNA sequence encoding human (secretory) II-5 receptor, which is synthesised from mRNA of human peripheral blood eosinophil; and an isolated human (secretory) II-5 receptor. Also claimed are a COS monkey cell transfected with a recombinant vector contg. the DNA; secretory human II-5 lacking a cytoplasmic and a content of the DNA; secretory human II-5 lacking a cytoplasmic and a content of the DNA; secretory human II-5 lacking a cytoplasmic and a content of the DNA; secretory human II-5 lacking a cytoplasmic and a content of the DNA; secretory human II-5 lacking a cytoplasmic and a content of the DNA; secretory human II-5 lacking a cytoplasmic and cytoplasmic and cytoplasmic and cytoplasmic and cytoplasmic and cytoplasmic and 
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11-SEP-1990; JP-240638.
(TAKA/) TAKATSU K.
Takatsu K, Tominaga A, Takagi S, Murata
WPI; 92-090329/12.
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DEKISLLPPVNFTIKVTG-LAQVLLQWKPNPDQEQ-RNVNLEYQVKINAPKEDDYETRIT 82
                                                   DTEIKVNPPQDFEIVDPGYLGYLYLQWQPPLSLDHFKECTVEYELKYRNIGSETWKTIIT 86
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                                                                                                        Conservative
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Pred. No. 6.8e<sup>o</sup>
69; Mismatches
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                                                                                                                                                                                                               Disclosure; Page 51; 65pp; English.

The inventors claim: an isolated cDNA sequence encoding murine (secretory) interleukin-5 (IL-5) receptor, which is synthesised from murine early B cell mRNA; an isolated murine (secretory) IL-5 receptor; an isolated cDNA sequence encoding human (secretory) IL-5 receptor, which is synthesised from mRNA of human peripheral blood eosinophil; and an isolated human (secretory) IL-5 receptor. Also claimed are a COS monkey cell transfected with a recombinant vector contg. the DNA; secretory human IL-5 lacking a cytoplasmic and a transmembrane region; and an expression vector.
                                                                                                                                                                                                                                                                                                                                                                                         Human and murine interleukin-5 for treatment of auto-immune ar
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11-SEP-1991
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ES---KCVTILHKGFSASVRTILQ---NDHSLLASSWASAELH-APPGSPGTSVVNLTCT
                             KNLHYKDGFDLNKGIEAKIHTLLPWQCTNGSEVQSSWAETTYWISPQGIPETKVQDMDCV 146
                                                            DEKISLLPPVNFTIKVTG-LAQVLLQWKPNPDQEQ-RNVNLEYQVKINAPKEDDYETRIT
                                                                                         DYEIKVNPPODFEIVDPGYLGYLYLOWOPPLSLDHFKECTVEYELKYRNIGSETWKTIIT 86
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Pred. No. 6.2e-22;
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밁	γQ	뭥	Qy	ઠ	δÃ	B	Ş	밁	Qy
362	363	309	309	250	249	190	192	136	147
362 CKICHLWIKLEP 373	363 LRKPNTYPKMIP 374	309 RAAVSSMCREAGLWSEWS-OPIYVGNDEHKPLREWFVIVIMATICFILLILSLI 361	309 RSKVNIYCSDDGIWSEWSDKQCWEGEDLSKKTLLRFWLPFGFILILVIFVTGLL 362	250 EGT-RLSIQMEKPVSAFPIHCFDYEVKIHNTRNGYLQIEKLMTNAFISIIDDLSKYDVQV 308	249 ESSCEIKLKWSIPLGPIPARCEDYEIEIREDDTTLVTATVENETYTLKTTNETRQLCEVV 308	190 LGRNIACWEPRTEILSKGRDWLAVLVNGSSKHSAIRPEDQLEALHAIDQINPPLNVTAEI 249	192 -GQNIGCREPYLEASDYKDFYICVNGSSENKPIRSSYFTFQLQNIVKPLPPVYLTFTR 248	136 INTTEDNYSRLRSYQVSLHCTWLVGTDAPEDTQYFLYYRYGSWTEECQEYSKDT 189	147YYNWQYLL-CSWKPGIGVLLDTNYNLFYWYEGLDHALQCVDYIKAD 191

Search completed: January 19, 2000, 20:00:50 Job time: 8945 sec

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GenCore version 4.5 Copyright (c) 1993 - 1998 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 19, 2000, 13:58:11; Search time 71.05 Seconds (without alignments) 252.278 Million cell updates/sec

Title:
Perfect score:
Sequence:

US-09-077-817-2
2104
1 MAFYCLAIGCLYTFLISTTF.....LLLRKPNTYPKMIPEFFCDT 380

Scoring table: BLOSUM62

Searched: 142080 segs, 47169319 residues

Database : PIR\_62:\*

Word size : 0

Number of hits that pass the threshold :

1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\* 142080

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

32 34 35	27 28 30 31	0 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	12 11 12 12 10	111 111 111 111	Result No.
131.5 129 126.5 122.5	134.5 133.5 133.5	160.5 159 159 151 151 150.5 149	170.5 178 165 165 165	292 263 247 220 216.5 212.5 212.5	Score 311.5 311.5
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prolactin receptor lactogen receptor membrane glycoprot granulocyte-macrop	granulocyte-macrop interleukin-3 rece leukemia inhibitor granulocyte-macrop granulocyte-macrop	prolactin receptor prolactin prolactin processor	н нын	interleukin-5 rece prolactin receptor interleukin-5 rece interleukin-2 rece prolactin receptor interleukin-2 rece interleukin-3 rece	

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638	638	918	26926	6805	1557	1630	863	771	783	•
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S04530	A33991	A44257	I38344	S20901	D41214	C41214	C38252	B38252	<b>JH0329</b>	
somatotropin recep	somatotropin recep	interleukin-6 sign	titin, cardiac mus	titin - rabbit (fr	protein-tyrosine-p	protein-tyrosine-p	granulocyte colony	granulocyte colony	granulocyte colony	

# ALIGNMENTS

Qy 309 RSKVNIYCSDDGIWSEWSDKQC	Cy 749 ESSCEIKLKWSIPLGPIPARCE	192 -	Q: 347YYNWQYLL-CSW 136 TNTTFDNYSRLRSYQVSLHCTW	Qy 87 KNLHYKDGFDLNKGIEAKHTILL :     :    :    :    :    :    :    :	Qy 27 DTEIKVNPPQDFEIVDPGYLGY	Query Match East Local Similarity 26.9%; Matches 100; Conservative 6	RESULT 1  \$21052  Interleukin-5 receptor alpha chain precursor (clone lambda h. f. Species: Homo sapiens (man)  C; Species: 1933 #sequence_revision 10-Nov-1995 #text_cha. (c) Pate: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_cha. (c) Pate: S21052; A46175  R; Mirata, X; Takaki, S; Migita, M.; Kikuchi, X; Tominaga, Y. Exp. Med. 175, 341-351, 1992  A; Fittle: Molecular cloning and expression of the human inter P; Reference number: S21050; MUID: 92121815  A; Accession: \$21052  A; Fitle: Later to the fittle fittl	
RSKYNIYCSDDGIWSEWSDKQCWEGEDLSKKTLLRFWLPFGFILILVIFVTGLL 362	ESSCEIKLKWSIPLGPIPARCFDYEIEIREDDTTLVTATVENETYTLKTTNETRQLCFVV 308   : ::   :        :::  :: : : : : :     EGT-%LSIQWEKPVSAFPIHCFDYEVKIHNTRNGYLQIEKLMTNAFISIIDDLSKYDVQV 308	-GQNIGGEPYLEASDYKDFYICVNGSSENKPIRSSYFTFQLQNIVKPLPPVYLTFTR 248 	YYNWQYLL-CSWKPGIGVLLDTNYNLFYWYEGLDHALQCVDYIKAD 191	KNLHYKDGFDLNKGIBAKIHTLLPWQCTNGSEVQSSWAETTYWISPQGIPETKVQDMDCV 146 ::    :	DTEIKVNPPODFEIVDPGYLGYLYLQWQPPLSLDHFKECTVEYELKYRNIGSETWKTIIT 86   :  :  :            :        :  :      :  :	Score 311.5; DB 2; Length 420; Pred. No. 2.3e-17; 69; Mismatches 156; Indels 47; Gaps 16;	ESULT 1  21052  21052  TherLeukin-5 receptor alpha chain precursor (clone lambda h5R.12), membrane-anchored Species: Homo sapiens (man)  Frate: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 20-Feb-1998  Rocession: S21052; A46175  Exp. Med. 175, 341-351, 1992  Filte: Molecular cloning and expression of the human interleukin 5 receptor.  Reference mimbr: S21050; MUID:92121815  Accession: S21050  Filte: Molecular voloning and expression of the human interleukin 5 receptor.  Reference mimbr: S21050; MUID:92121815  Accession: S21050; MUID:92121815  Accession: S21050; MUID:92121815  Accession: S21050; MUID:92121815  Filte: Molecular voloning and expression of the human interleukin 5 receptor.  Reference nimbr: S21050; MUID:92121815  Filte: Molecular voloning and expression of the human interleukin 5 receptor.  Reference nimbr: S21050; MUID:92121815  Filte: Molecular voloning and expression of the human interleukin 5 receptor.  Residus: 1.420 <mur>  Cross: reference: Clone lambda h5R.12  Tavernier: J: Tuypens; T: Plaetinck, G:; Verhee, A:: Fiers, W:; Devos, R.  Toc. Natl. Acad. Sci. U.S.A. 89, 7041-7045, 1992  Title: Molecular voloning and expression of the human reference number: A46175  Molecular voloning and expression of the human reference number: A46175  Experimental source: HL-60 cells and eosinophils  Note: Sequence extracted from NCBI backbone (NCBIN:116243, NCBIP:116244)  Molecular voloning and expression of the human receptor: glycoprotein; transmembrane prot 12-30/Towaln: signal sequence #status predicted (MAT)  1.53/Domain: transmembrane #status predicted (Man)  1.53/S.151.137,142,216,244/Blanding site: carbohydrate (Asn) (covalent) #status predicte</mur>	ALIGNMENTS

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J. Exp. Med. 175, 341-351, 1992
A;Title: Molecular cloning and expression of the human interleukin 5 receptor A; Acference number: $21050; MUID:92121815
A;Molecular clonic $21050
  interleukin-5 receptor precursor,
C;Species: Homo sapiens (man)
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A;Residues: 1-128,/I',/130-396 <MUM>
A;Residues: 1-128,/I',/130-396 <MUM>
A;Cross-references: EMBL:X61177; NID:g33839; PID:g33840
A;Cross-references: EMBL:X61177; NID:g33839; PID:g33840
C;Keywords: alternative splicing; cytokine receptor; glycoprotein; transmembrane
F;1-20/Domain: signal sequence #status predicted <SIG>
F;21-396/Product: interleukin-5 receptor alpha chain #status predicted <MAT>
F;345-365/Domain: transmembrane #status predicted <MAT>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: EMBL:X61177; NID:g33839; A;Experimental source: clone lambda h5R.27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        nterleukin-5 receptor alpha chain precursor (clone lambda h5R.27) - human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Species: Homo sapiens (man)
Date: 29-Jan-1998 #sequence_revision 06-Feb-1998 #text_change 05-Jun-1998
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Best Local
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                                                                                                                                                                                                            RAAVSSMCREAGLWSEWS-QPIYVGNDEHKP--LREW----FVIVIMATICFILLILSLI
                                                                                                                                                                                                                                                  RSKVNIYCSDDGIWSEWSDKQCWEGEDLSKKTLLRFWLPFGFILIL-----VIFVTGLL
                                                                                                                                                                                                                                                                                                                                 ESSCEIKLKWSIPLGPIPARCFDYEIEIREDDTTLVTATVENETYTLKTTNETRQLCFVV
                                                                                                                                                                                                                                                                                                                                                                            LGRNIACWFPRTFILSKGRDWLAVLVNGSSKHSAIRPFDQLFALHAIDQINPPLNVTAEI 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ES---KCVTILHKGFSASVRTILQ---NDHSLLASSWASAELH-APPGSPGTSVVNLTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KNIHYKDGFDLNKGIEAKIHTLLPWQCTNGSEVQSSWAETTYWISPQGIPETKVQDMDCV 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DTEIKVNPPQDFEIVDPGYLGYLYLQWQPPLSLDHFKECTVEYELKYRNIGSETWKTIIT 86
                                                                                                                                                                                                                                                                                                                                                                                                                  -GQNIGCRFP--YLEASDYKDFYICVNGSSENKPIRSSYFTFQLQNIVKPLPPVYLTFTR 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DEKISLLPPVNFTIKVTG-LAQVLLQWKPNPDQEQ-RNVNLEYQVKINAPKEDDYETRIT 82
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Pred. No. 2.2e-17;
                     soluble (clone lambda h5R.25)
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Query Match
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C; Date:
C; Access
                                                                                                                                                                                                                                                         C; Species: Homo sapiens (man) • C; Date: 17-Jan-1992 #sequence_revision
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C;Keywords: alternative splicing; Cytokine receptor; glycoprotein
F;1-20/Domain: signal sequence #status predicted <SIG>
F;21-33/Product: interleukin-5 receptor #status predicted <MAT>
F;35,131,137,142,216,244/Binding site: carbohydrate (Asn) (covalent)
A; Cross-references: GB:M75914; C; Keywords: cytokine receptor;
                                                                                                                A; Reference number: A40267; A; Accession: A40267
                                                                                                                                                                                  Cell 66, 1175-1184, 199
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A;Title: Molecular cloning and expression of the human interleukin 5 receptor
A;Reference number: 821(50; MUID:92121815
                                                 A; Molecule type: mRNA
A; Residues: 1-335 <TAV>
                                                                                                                                                               A; Title: A human high affinity interleukin-5 receptor
                                                                                                                                                                                                            R; Savernier,
                                                                                                                                                                                                                                 C; Accession: A40267
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                                                                                           A; Status: preliminary
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A;Residues: 1-128,'I',130-333 <MUW>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A, Residues:
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                                                                                                                                                                                                                                                                                                   interleukin-5 receptor alpha chain precursor -
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Experimental source: clone lambda h5R.25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Y.; Takaki, S.; Migita, M.; Kikuchi, Y.; ed. 175, 341-351, 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RSKVNIYCSDDGIWSEWS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LGRNIACWEPRTFILSKGRDWLAVLVNGSSKHSAIRPFDQLFALHAIDQINPPLNVTAEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -GQNIGCRFP--YLEASDYKDFYICVNGSSENKPIRSSYFTFQLQNIVKPLPPVYLTFTR 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -----YYNWQYLL-CSWKPGIGVLLDTNYNLFY----WYEGLDHALQCVDYIKAD 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KNLHYKDGFDLNKGIEAKIHTLLPWQCTNGSEVQSSWAETTYWISPQGIPETKVQDMDCV 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DEKISLLPPVNFTIKVTG-LAQVLLQWKPNPDQEQ-RNVNLEYQVKINAPKEDDYETRIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DTEIKVNPPQDFEIVDPGYLGYLYLQWQPPLSLDHFKECTVEYELKYRNIGSETWKTIIT
                                                                                                                                                                                                                                                                                                                                                                                                                    RAAVSSMCREAGLWSEWS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EGT-RLSIQWEKPVSAFPIHCFDYEVKIHNTRNGYLQIEKLMTNAFISIIDDLSKYDVQV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ESSCEIKLKWSIPLGPIPARCFDYEIEIREDDTTLVTATVENETYTLKTTNETROLCFVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TNTTEDNYSRLRSYQVSLHCTWLVGTDAPEDTQYFLYYRYGSWTE-----ECQEYSKDT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ES----KCVTILHKGFSASVRTILQ----NDHSLLASSWASAELH-APPGSPGTSVVNLTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1-333 <MUR>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                            Devos,
                                                                                                                                                                                                            R.; Cornelis, S.; Tuypens, T.; Van der Heyden, J.; Fiers,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13.9%;
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                                                                                                                                          MUID: 92005669
                                                                                                                                                                                                                                                                                                                                                                                                                                                              326
                                                                                                                                                                                                                                                                                                                                                                                                                    326
    NID:g186387; PID:g186388 transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     55;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 293; DB 2;
Pred. No. 5.1e-16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       September
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
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                                                                                                                                                                                                                                                      17-Jan-1992 #text_change 10-Sep-1997
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13.9%;

Score Pred.

292; DB 2; No. 6.2e-16;

Length

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C:Keywords: glycoprotein; transmembrane protein
F;1-23/Domain: signal sequence #status predicted <SIG>
F;24-831/Product: prolactin receptor #status predicted <MAT>
F;439-462/Domain: transmembrane #status predicted <TMM>
F;549-462/Domain: transmembrane #status predicted <TMM>
F;59,91,100,112,132,262,303,315,335,647,701,800/Binding site: carbohydrate (Asn) (coval
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Molecule type: mRNA
A;Residues: 1-831 <TAN>
A;Cross-references: DDBJ:D13154; NID:g222848; PID:d1002939;
A;Experimental source: kidney
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Accession: JQ1655
R;Tanaka, M.; Maeda, K.; Okubo, T.; Nakashima, K.
Biochem. Biophys. Res. Commun. 188, 490-496, 1992
A:Title: Double antenna structure of chicken prolactin
A;Reference number: JQ1655; MUID:93075121
A;Accession: JQ1655
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 prolactin receptor precursor - chicken C; Species: Gallus gallus (chicken) C; Date: 30-Sep-1993 #sequence_revision
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Best Local Similarity
Matches 103; Conserv
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                                     LPPVYLTFTRESSCEIK----LKWS-IPLGPIPARCFDYEIEIR---EDDTTLVTATVEN 290
                                                                                                                                                                          QSSWAETTYWISPQG-IPETKVQDMDCVYYNWQYLLCSWKPGIGVLLDTNYNLFYWYEGL 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RAAVSSMCREAGLWSEWS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TNTTEDNYSRLRSYQVSLHCTWLVGTDAPEDTQYFLYYRYGSWTE-----ECQEYSKDT 189
DPPVNVTLELKKPINRKPYLVLTWSPPPLADVRSGWLTLEYELRLKPEEGEEWETIFVGQ 390
                                                                         EQVYECPDY-RTAGPN-SCYFDKKHTSFWTIYNITVRATNEMGSNSSDPHYVDVTYIVQP
                                                                                                               DHALQCVDYIKADGQNIGCRFPYLEASDYKDFYICVNGSSENKPIRSSYFTFQLQNIVKP
                                                                                                                                                    WSEWSSERHILIPSGQSPPEKPTIIKCRSPEKETFTCWWKPGLDGGHPTNYTLLYSKEGE 272
                                                                                                                                                                                                                            DASSNHLYHYELRIKPEEKEEWETI----SVGVQTQCKINR-LNAGMRYVVQVRCTLDPGE 212
                                                                                                                                                                                                                                                               DHFKECTVEYELKYRNIGSETWKTIITKNLHYKDGFDLNKGIEAKIHTLLPWQCTNGSEV 119
                                                                                                                                                                                                                                                                                                       TTFNITVTATNEIGSNSSDPQYVDVTSIVQPGSPVNLTLETKRSANIMYLWAKWSPPLLA 156
                                                                                                                                                                                                                                                                                                                                             TTFGCTSSSDTEIKVN--PPQDFE---IVDPG----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RSKVNIYCSDDGIWSEWS 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EGT-RLSIQWEKPVSAFPIHCFDYEVKIHNTRNGYLQIEKLMTNAFISIIDDLSKYDVQV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -----YYNWQYLL-CSWKPGIGVLLDTNYNLFY----WYEGLDHALQCVDYIKAD 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ES---KCVTILHKGFSASVRTILQ---NDHSLLASSWASAELH-APPGSPGTSIVNLTCT
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                                                                                                                                                                                                                                                                                                                                                                              12.5%; Score 263; DB 2; 26.4%; Pred. No. 3.8e-13; tive 58; Mismatches 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        326
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                                                                                                                                                                                                                                                                                                                                             ----YLGYLYLQWQPPLSL 59
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                                                                                                                                                                                                                                                                                                                                                                                                                    Length 831;
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R:Takeshita, T.; Asao, H.; Ohtani, K.; Ishi
Science 257, 379-382, 1992
A:Title: Cloning of the gamma chain of the
A:Reference number: A42565; MUID:92335883
                                                                                                                             interleukin-2 receptor gamma chain - human
C;Species: Homo sapiens (man)
C;Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 23-Jul-1999
C;Accession: A42565; A46591; I54332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                interleukin-5 receptor - mouse
C:Species: Mus musculus (house mouse)
C:Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 20-Mar-1998
                    A;Reference number:
Accession: A42565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: GB:D90205; C;Keywords: cytokine receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; filtle: Molecular cloning a A; Reference number: S12357;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R:Takaki, S.; Tominaga,
EMBO J. 9, 4367-4374, 1
A.Status: preliminary; not compared with conceptual translation
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A; Residues: 1-415 <TAK>
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                  306 RAAVSSPCRMPGRWGEWS-QPIYVGKE--RKSLVE-WHLIVLPTAACFVLLIF--SLICR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                198
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                                                                                                                                                                                                                                                                                                                                                         SES KPNTYPKMIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  140. HTHLRPYQVSLRCTWLVGKDAPEDTQYFLYYRFGVLTE--KCQEYSRDALNRNTACWFPR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                444 VLGVLSSLICLIMSWTMVLKGYRMITFMLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           29. ET-YTLKTTNETROLCFVVRSKVNIYCSDD--GIWSEWSDKQCWE-GEDLSKKTLLREWL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             150 ----- WOY-LLCSWKPGIGVLLDTNYNLFYWYEGLDHALQCVDYIK-ADGQNIGCRFP-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         84 VTPLHEGFAASVRTILK---SSHTTLASSWVSAEL-KAPPGSPGTSVTNLTCTTHTVVSS
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                                                                                                                                                                                                                                                                                                             VCHLWTRLFP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KPLSAFPDHCFNYELKIYNTKNGHIQKEKLIANKFISKIDDVSTYSIQ------V
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TETMSKGFEQLAVHINGSSKRAAIKPFDQLFSPLAIDQVNPPRNVTVEIESN-SLYIQWE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GFULNKGIEAKIHTLLPWQCTNGSEVQSSWAETTYWISPQGIPETKVQDMDCVYYN----
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                                                                                                                                                                                                                                                                                                                                                                                                                                           REKVNIYCSDDGIWSEWSDKQCWEGEDLSKKTLLRFW----LPF@FILILVIFVTGLLLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PPVNFTIKATG-LAQVILHWDPNPDQEQ-RHVDLEYHVKINAPQEDEYDTRKTES---KC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -YLEASDYKDFYICVNGSSENKPIRSSYFTFQLQNIVKPLPPVYLTFTRESSCEIKLKWS
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1990
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NID:g220465; PID:d1014936; PID:g220466 transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  70;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 247; Ub ...
No. 3e-12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
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                                                                                                           Ishii,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                473
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                                                             receptor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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type: nucleic

acid;

protein

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prolactin receptor - pigeon
C;Species: Columba livia (domestic pigeon)
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 13-Sep-1996
C;Accession: I50455
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J. Biol. Chem. 268, 13601-13608, 1993
A:Title: Characterization of the human interleukin-2 receptor A:Reference number: A46591; MUID:93293887
A:Accession: A46591
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A; Note: defects are associated with an X-linked form of severe combined
C; Superfamily: interleukin-2 receptor gamma chain
C; Keywords: cytokine receptor; duplication; immunodeficiency; severe com
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Gene: GDB:IL2RG; SCIDX1; IMD4
A;Cross-references: GDB:134807; OMIM:308380
A;Map position: Xq13.1-Xq13.1
                                                                                    A; Status: preliminary; translated
                                                                                                                                     A; Title: Cloning, expression, and mutational analysis A; Reference number: I50455; MUID:94283267
                                                                                                                                                                                                                    R; Chen, X.; Horseman, N.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Title: The interleukin-2 receptor gamma chain maps to Xq13.1 and A;Reference number: I54332; MUID:94004847 A;Accession: I54332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: GB:L12183; NID:g307056; PIDN:AAA59145.1; PID:g307058 R;Puck, J.M.; Deschenes, S.M.; Porter, J.C.; Dutra, A.S.; Brown, C.J.; Willard, Hum. Mol. Genet. 2, 1099-1104, 1993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Residues: 1-369 < 1
A; Cross-references:
A;Cross-references: EMBL:U07694; NID:g466381; PID:g466382
                                                                                                                                                                                         Endocrinology 135,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Experimental source: MOLT
                                                                                                               A; Accession: I50455
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                                      Residues: 1-830 <CHE>
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         73 TWNSSSEPQP-----TNLTLHYWYKNSDNDKVQKCSHYLFSEEITSGCQLQKKEIHLY 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KDFYICVNGSSENKPIRSSYFTFQLQNIVKPLPPVYLTFTRESSCEIKLKWSIPLGPIPA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SDKQCWEGEDLSKKTLLRFWLPFGFILILVIFVTG 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HCLEHLVQYRTDWDHSWTEQSVDYRHKFSLPSVDGQKRYTFRVRSRFNPLCGSAQHWSEW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LGVGLNTTILT-----PNGNEDTTADFFLTTMPTDSLSVSTLPLPEVQCFVFNVEYMNC 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LNKGIEAKIHTLLPWQCTNGSE-VQSSWAETTYWISPQGIPETKVQDMDCVYYNWQYLLC 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       type: DNA
: 1-369 <RE2>
                                                              type: mRNA
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                                                                                                                                                                                           269-276, 1994
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                                                                                 from GB/EMBL/DDBJ
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Pred. No. 3.5e-10;
3; Mismatches 121
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                                                                                                                                                                얁
                                                                                                                                                           the pigeon prolactin receptor.
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                                                                                                                                                                                                                                                                                    207
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                                 338 KKTLLRFWLPFGFILILVIFV 358
                                                                                                                                                                                                               267 LYSKEGEERVYECPDY-KTAGPN-SCYFDKKHTSFWTIYNITVKATNEIGSNVSDPLYVD
                                                                                                                                                                                                                                                                                                                                                                                               54
                                                                                                                                                                                                                                                                                                                                                                                                                                97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18 TTFGCTSSSDTEIKVNPPQDFEIVDPGYLG------
IKDMV-VWIIVGVLSSLICLV 456
                                                                                                                                          VTYIVQTDPPVNVTLELKKTVNRKPYLVLTWSPPPLADVRSGWLTLDYELRLKPEEA---
                                                                                                                                                                             LQNIVKPLPPVYLTFTRESSCEIK----LKWS-IPLGPIPA--RCFDYEIEIREDDTTLV
                                                                                                                                                                                                                                     FYWYEGLDHALQCVDYIKADGQNIGCRFPYLEASDYKDFYICVNGSSENKPIRSSYFTFQ
                                                                                                                                                                                                                                                                                                                                                           SPPPLADVTSNSHVYRYELRLKPEEKEEWETV---SVGVQTQYKVNR-LQAGVKYVVQVR
                                                                                                                                                                                                                                                                                                                                                                                             QPPLSLDHFKECTV-EYELKYRNIGSETWKTIITKNLHYKDGFDLNKGIEAKIHTLLPWQ 112
                                                                                                      TATVENETYTLKTTNETROLCFVV----RSKVNIYCSDD--GIWSEWS-DKQCWEGEDLS
                                                                                                                                                                                                                                                                                      CVLDIGEWSEWSSERHIHIPNGESPPEKPTIIKCRSPEKETFTCWWKPGSDGGHPTNYTL
                                                                                                                                                                                                                                                                                                                    CINGSEVQSSWAETTYWISPQG-IPETKVQDMDCVYYNWQYLLCSWKPGIGVLLDINYNL 171
                                                                                                                                                                                                                                                                                                                                                                                                                              TTYNITYMAMNEIGSNSS-----DPQYVDVTSIVQPDAPVNLSLETKTSASTTYLLAKW 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10.3%;
Similarity 24.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 216.5; DB 2
Pred. No. 1.9e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 830;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -----YLYLQW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                    266
                                                                                                                                                                                                                                                                                                                                                             206
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                                                                                                                                          382
                                                                                                                                                                             284
                                                                                                                                                                                                                                                 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16;
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inéc:leukin-2 receptor gamma chain precursor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 27-reb-1997 #sequence_revision 27-Feb-1997 #:
C;Accession: I49280; A47514; JN0592; JN0775; S37582;
                                                                                                                                                                                  R;Cao; X; Kozak, C.A.; Liu, Y.
Proc. Natl. Acad. Sci. U.S.A. 90, 8464-8468,
A;Title: Characterization of cDNAs encoding
                                                                      A; Molecule type: DNA
A; Residues: 1-369 <CAO>
                     A;Cross-references: EMBL:U21795; NID:g727349; A;Accession: A47514
                                                                                                                     A;Status:
                                                                                                                                      Reference number: A47514; Accession: I49280
Status: translated from GB/EMBL/DDBJ
                                                                                                                preliminary;
                                                                                                                translated
                                                                                                                                                                   MUID:93391374
                                                                                                                from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                           27-Feb-1997 #text_change
N0775; S37582; I53398
                                                                                                                                                                                       the
                                           PIDN: AAA64279.1;
                                                                                                                                                                                       murine
                                                                                                                                                                                       interleukin
                                           PID: g727350
                                                                                                                                                                                       N
                                                                                                                                                                                       receptor
                                                                                                                                                                                    (IL-2R)
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A; Molecule type: mRNA A; Residues: 1-369 < KO

1-369 <KOB>

A;Cross-references: GB:D13821; NID:g436045; R;Chiu, R.K.; Dougherty, G.J.

submitted to the EMBL Data Library,

October 1993

PIDN:BAA02974.1;

PID:d1003480; PID:g43604

Gene 130,

303-304, 1993

R; Kobayashi

A; Residues: 1-369 < KUM>

A; Molecule type: mRNA

A; Status: nucleic acid sequence not shown

A; Reference number: JN0592; A; Accession: JN0592

Kumaki, S.; Kondo, M.; Takeshita, T.; Asao, H.; Na iochem. Biophys. Res. Commun. 193, 356-363, 1993 /Title: Cloning of the mouse interleukin 2 receptor

MUID:93277575

Cross-references: GB:L20048; NID:g404067; PIDN:AAA39286.1; PID:g404068

Nakamura,

chain: . .

Demonstration

of fu A; Molecule type: mRNA

1-369 <RE2>

A; Title: Cloning and sequencing of the cDNA encoding a mouse IL-2 A; Reference number: JN0775; MUID:93366191 A; Accession: JN0775

Cross-references: DDBJ:D13565; NID:g303684; PIDN:BAA02760.1; PID:d1003265; PID:g303 Kobayashi, N.; Nakagawa, S.; Minami, Y.; Taniguchi, T.; Kono, T.

duplication

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                                                                                                                                                  R;Henthorn, P.S.; Somberg, R.L.; Fimiani, V.M.; Puck Genomics 23, 69-74, 1994
A;Title: II-2Rgamma gene microdeletion demonstrates A;Reference number: A55718; MUID:95130114
A;Accession: A55718
                                                                                                                                                                                                                                                                                                                                                                      interleukin-2 receptor gamma chain precursor - C;Species: Canis lupus familiaris (dog) C;Date: 18-Aug-1995 *sequence_revision 18-Aug-1995 *sequence_revisio
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A; Reference number:
A; Accession: S37582
A; Residues: 1-373 <HEN>
A; Cross-references: GB:
C; Superfamily: interleu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Pathway: interleukin-2 stimulated growth and differentiation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Introns: 39/1; 90/2; 152/1; 199/3; 254/1; 286/2; 308/3
C;Complex: The high affinity receptor is a heterotrimer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Residues:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: mRNA
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Genetics:
                                                                                                                                Status: preliminary
                                                                                                                                                                                                                                                                                                                                   Accession:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PETKVQDMDCVYYNWQYLLCSW----KPGIGVLLDTNYNLFYWYEGLDHAL--QCVDYIK 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LLRKPNTYP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LERMPPIPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VRSKVNIYCSDDGIWSEWSDKQCWEG----EDLSKKTLLRFWLPFGF--ILILVIFVTGL 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SESQLELRWK--SRHIKERCLQYLVQYRSNRDRSWTELIVNHEPRFSLPSVDELKRYTFR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SSCEIKLKWSIPLGPIPARCFDYEIEIRED-DTTLVTATVENE-TYTLKTTNETRQLCFV 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SKEITSGCQIQKEDIQLYQTFVVQL--QDPQKPQRRAVQKLNLQNLVIPRAPENLTLSNL 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADGQNIGCRFPYLEASDYKDFYICVNGSSENKPIRSSYFTFQLQNIVKPLPPVYLTFTRE 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PTLPLPEVQCFVFNIEYMNCTWNSSSEPQA----TNLTLHYRYKVSDNNTFQECSHYLF 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   preliminary
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   interleukin-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                    Somberg, R.L.; Fimiani, V.M.; Puck, J.M.; Patterson, D.F.;
GB:U04361; NID:g517411; rleukin-2 receptor gamma
                                                                                                                                                                                                                                                                                                                                                                   #sequence_revision
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GB:S75852; NID:g861554; PIDN:AAB32904.1;
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Pred. No. 1.4e-09;
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   PIDN:AAC48403.1;
chain
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                               PID:g517412
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 283
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                                                                                                                                                                                                                                                                                                    Felsburg,
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G:Superfamily: interleukin-3 receptor beta chain; cytokine r (Neywords: Gytokine receptor; gupilcation; transmembrane pr F;1-22/pomain: signal sequence #status predicted <SIG> F:23-878/Product: interleukin-3 receptor beta chain #status
                                                                                                                                                                                                                                                                                                                                                                                                                                             F:254-433/Domain: cytokine receptor homology <CRS2>
F:441-462/Domain: transmembrane #status predicted <INT>
F:463-578/Domain: intracellular #status predicted <INT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A://olecule type: mRNA
A;//asidues: 1-915;/0',817-878 <GOR>
A;//asidues: 1-915;/0',817-878 <GOR>
C;/Comment: In mice there are two classes of high-affinity IL-3 receptors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            δ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R; Jtoh, N.; Yonehara, S.; Science 247, 324-327, 1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C; Accession: A40091; A4302;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C:Date: 30-Jun-1993 #sequence_revision
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C; Species: Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     F:23-440/Domain: extracellular *status predicted <EXT>F:39-236/Domain: cytokine receptor homology <CRS1>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 P. Gorman,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ü
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             submitted to GenBank, November
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Reference number: A40091; MUID:90117145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Title: Cloning of an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     interleukin-3 receptor beta chain precursor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Accession: A430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A:Reference number:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Mclecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; succession: A40091
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
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194 -TSNFQVN--LEPKL--FLPNSIYAARVRTRLSAGSSLSGRPSRWSPEVHWDSQPG-DKA 247
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                                                             91 YKDCFDLNKGIEAKIHTLLP------WQCTNGSEVQ---SSWAFTTYWISPQGIPET 138
                                                                                                                                                                                                                                                                                                           Local Similarity
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                                                                                                                                     PPKDIHISPSG--DHFLLEWSVSLGDSQVSWLSSKDIEFEVAYKRL-QDSWED--ASSLH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NKPIRSSYFTFQLQNIVKPLPPVYLTFTRESSCEIKLKWSIPLGPIPARCFDYEIEIRED
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NGSE-----VQSSWAETTYWISPQGIPETKVQDMDCVYYNWQYLLCSW-----KPGI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          not
                                                                                                                                                                                                                                                                              59;
                                                                                                                                                                                                                                                                          Score 195; DB 1;
Pred. No. 1e-07;
9; Mismatches 150
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Pred. No. 3.2e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               358
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                                                                                                                                                                                                                                                                              150;
                                                                                                                                                                                                                                                                                                                                        Length 878
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22-Jun-1999
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A; Map position: 22q13.1-22q13.1

Q; Superfamily: interleukin-3 receptor beta chain; cytokine receptor homology C; Reywords: alternative splicing; cytokine receptor; duplication; transmembra E;1-16/Domain: signal sequence #status predicted <SIG>
E;17-897/Product: cytokine receptor common beta chain #status predicted <MATS F;17-897/Promain: extracellular #status predicted <EXTS F;17-443/Domain: cytokine receptor homology <CRS1>
E;35-323/Domain: cytokine receptor homology <CRS1>
E;35-323/Domain: cytokine receptor homology <CRS2>
E;444-460/Domain: transmembrane #status predicted <TMMS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 12
A39255
Cytokine receptor common beta chain precursor - human
C;Species: Homo sapiens (man)
C;Date: 30-Jun-1993 *sequence_revision 30-Jun-1993 *text_change 02-Sep-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C:Accession: A39255
R:Hayashida, K.; Kitamura, T.; Gorman, D.M.; Arai, K.; Yokota, Proc. Natl. Acad. Sci. U.S.A. 87, 9655-9659, 1990
A;Title: Molecular cloning of a second subunit of the receptor A;Reference number: A39255; MUID:91088571
A;Accession: A39255
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A;Residues: 1-897 <HAY>
A;Cross-references: GB:M38275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Gene: GDB:CSF2RB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;Cross-references: GDB:126838;
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           IREDDTTLVTAT-VENETYTLKTTN----
                                                                                                                                                                                  VLLDTNYNLFYWYEGLDHALQCVDYIKADGQNIG-----CRFPYLEASDYKDFYICVN 215
                                                                                                                                                                                                                                                                         KIHT-LLPWQCTNGSEVQSSWAETTYWISPQGIPETKVQDMDCVYYNWQYLLCSWKPGIG 162
                                                                                                                                                                                                                                                                                                                     GSPQSHWLSPGDLEFEVYYKRL-QDSWEDAAILLSNTS-----QATLGPEHLMPSSTYVA 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VRVKPISDY---DGIWSEWSNEYTWT-TDWVMPTL---WI----VLILVFLIFTLLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VRSK-VNIYCSDDGIWSEWSDKQCWEGEDLSKKTLLRFWLPFGFILILVIFVTGLLL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IKLKWSIPLGPIPARCFD--YEIEIREDDTTLVTATVEN----ETYTLKTTNETRQLCFV 307
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QPQNLQCFFDGIQSLHCSWEVWTQTTGSVSFGLFYRPSPAAPEEKCSPVVKEPQASVYTR 307
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                                                                                             GSSENKPIRSSYFTFQLQNIVKPLPPVYLTFTRESSCEIKLKWSIPLGPIPARCFDYEIE 275
                                                                                                                                       VASSVSFGLFYKPSPDAGEEECSPVLR----EGLGSLHTRHHCQIPVPDPATHGQYIVSVQ
                                                                                                                                                                                                                                RVRTRLAPGSRLSGR--PSKWSPEVCWDSQPG-DEAQPQNLECFFDGAAVLSCSWEVRKE
                                                                                                                                                                                                                                                                                                                                                                                                         VIPCQSFVVTDVDYFSFQPDRPLGTRLTVTLTQHVQPPEPRDLQISTDQDHFLLTWSVAL 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  YRCSLPVPEPSAHSQYTVSVKHLEQGKFI-MSYYHIQME-----PPILNQTKNRDS---
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                                                    NI--QMAPPSLNVTKDGD-SYSLRWETMKMRYEHIDHTFEIQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                58;
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Pred. No. 1.5e
58; Mismatches
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         ETRQLCFV-VRSKVNIYCSDDGIWSE 324
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A; Gene: rIL-3Rbeta
C; Superfamily: inte
C; Keywords: cytokin
F; 39-235/Domain: cy
                                cytokine receptor common beta chain precursor cyspecies: Mus musculus (house mouse) cyspecies: O.C. Cytote: 30-Jun-1993 #sequence_revision 30-Jun-Cytocession: A35782
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C;Genetics:
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A; A:cession: I56563
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C:Date: 26-Jul-1996
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                  R; Gcrman, D.M.;
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A; Residues: 1-896 <RES>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Title: Cloning of rat interleukin-3 receptor beta-subunit from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        J. Neurosci. 15, 5800-5809,
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Best Local Similarity 21.4%;
Matches 87; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Superfamily: interleukin-3 receptor beta chain; Keywords: cytokine receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        39-235/Domain: cytokine receptor homology 253-433/Domain: cytokine receptor homology
                                                                                                                                                                                               422
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                                                                                                                                                                                                                                                                        366 MSYPFIQHAFQVQYKKKLDRWEDSKT----ENLNHAHSMDLPQLEPGTSYCARVRVKTIP
                                                                                                                                                                                                                                                                                                                                                                                                                               263
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                94 CVPRRCVLPYTQFSVSKEDYYSLQPDRDLSIHLVVPLAQHVQPPPPKDISISPSG--DHF
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                                                                                                                                                                                                                                                                                                                                                                              NGSSENKPIRSSYFTFQLQ------NIVKPLPP-VYLTFTRESSCEIKLKWSIPL
                                                                                                                                                                                             EYKGLWSEWSNECTWT-TDWVMPTL---WI----VLILVFLILTFLL
                                                                                                                                                                                                                               SDDGIWSEWSDKQCWEGEDLSKKTLLRFWLPFGFILILVIFVTGLLL 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LLKWSVPLGDAQVSLLSQKDIQFEVAYKQL-QDSWED--ASSLH-----TCNLWVTLEPK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLAIGCL--YT-FLISTTFGCTSSSDTEIKVN-----
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                                                                                                                                                                                                                                                                                                              GPIPARCFDYEIEIR-----EDDTTLYTATVENETYTLKTTNETRQLCFVVRSKVNIYC
                                                                                                                                                                                                                                                                                                                                                  NVSU----PAAHSQYTVSVKRLEQGKFIESFNHIQMNPPTLNLTKNRDS----YSLHWETQK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CSWKPGIGVLLDTNYNLFYWYEGLDHALOCVDYIKADGONIGCRFPYLEASDYKDFYICV
M.; Itoh, N.; Kitamura, T.; Schr
Acad. Sci. U.S.A. 87, 5459-5463,
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96 #sequence_revision 26-Jul-1996 #text_change
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                                                      30-Jun-1993 #text_change
                    Schreurs,
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                  J.;
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A; Titlé: Cloning and expression of a gene encoding

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                                                                                                                                                                                                                                                                                                                                                                                                                    ;Species: Bos primigenius taurus (cattle);Date: 16-Aug-1996 #text_change
                                                                                                                                                                           ;Cross-references:
                                                                                                                                                                                                                                                                                                           Scott, P.; Kessler, M.A.; Schuler, L.A.
ol. Cell. Endocrinol. 89, 47-58, 1992
of the bovine prolactin receptor and distribution of prolacting the state of the polacting property.
Query Match
Best Local Similarity
Matches 63; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Superfamily: interleukin-3
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Local Similarity 20.7%;
les 81; Conservative 6
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7.8%; Score 165; DB 2; 31.3%; Pred. No. 1.4e-05; ive 24; Mismatches 96
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9; Mismatches 185
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Search completed: January 19, 2000, 14:58:48
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GenCore version 4.5 Copyright (c) 1993 - 1998 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 20, 2000, 06:18:23; Search time 35.05 Seconds (without alignments) 315.340 Million cell updates/sec

Title: Perfect score: Sequence: US-09-077-817-2
2104
1 MAFYCLAIGCLYTFLISTTF .....LLLRKPNTYPKMIPEFFCDT 380

Searched: 80000 seqs, 29085965 residues Scoring table:

BLOSUM62

Database : SwissProt\_38:\*

Word size :

Number of hits that pass the threshold : 80000

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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O1344;
O1-301-44;
O1-JUL-1993 (Rel. 26, Created)
O1-JUL-1993 (Rel. 26, Last sequence update)
O1-NOV-1997 (Rel. 35, Last annotation update)
O1-NOV-1997 (Rel. 35, Last annotation precursor (IL-5R-ALPHA) (CD125)
           TAVERNIER J., DEVOS R., FIERS W., PLAETINCK G.;
                                 SEQUENCE OF 1-335 FROM N.A. MEDLINE; 92005669.
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Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eukaryota; Primates; Catarrhini; Hominidae; Homo.
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SEQUENCE
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                                                                                                                                                       SCOTT H.S., GUO X.H., HOPWOOD J
"Structure and sequence of the ]
Genomics 13:1311-1313(1992).
                                                                                                                                                                   "SCOTT H.S., GUO X.H.,
                                                              Molecular basis of the membrane-anchored and two the human interleukin 5 receptor alpha subunit."; proc. Natl. Acad. Sci. U.S.A. 89:7041-7045(1992).
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Pred. No. 6.7
0; Mismatches
                                                                                                                                                              .J., MORRIS C.P.;
human alpha-L-iduronidase gene.
                                                                                                            VERHEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CRC32;
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5.7e-157;
                                                                                                           Α.,
                     VAN
                                                                                    soluble isoforms
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                    DER HEYDEN
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Best Local :
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EMBL; M96651; AAA59151.1; -
EMBL; M75914; AAA36110.1; -
EMBL; A26249; CAA01793.1; -
EMBL; A26251; CAA01794.1; -
                                                                                                                                                                                                                                                                                                       CARBOHYD
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CARBOHYD
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DOMAIN
CARBOHYD
                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE; PS00241; RECEPTOR_CYTOKINES_1; PROSITE; PS00340; RECEPTOR_CYTOKINES_2; Receptor; Transmembrane; Glycoprotein; I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               use by non-profit institutions as long as its content modified and this statement is not removed. Usage by an entities requires a license agreement (See http://www.isb-or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Ew the European Bioinformatics Institute. There are no restr
       190
                                                                                                                                                                                                                                                                                                                                                                                                                                               DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SIGNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    an IL5-specific alpha chain and
for GM-CSF.";
                                                                                                                                                                    25
                                                                                                                                                                                               27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE SPECIFICITY: EXPRESSED ON EOSINOPHILS AND BASO:
SIMILAPITY: BELONGS TO THE CYTOKINE FRMILY OF RECEPTO:
SIMILARITY: TO IL-13 RECEPTOR ALPHA-2 CHAIN.
DATABASE: NAME-PROW; NOTE-CD guide CDw125 entry;
WWW-"http://www.ncbi.nlm.nih.gov/prow/cd/cdw125.htm".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CHAIN IS COMMON TO THE IL-3, IL-5 AND GM-CSF RECEPTORS.
SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
ALTERNATIVE PRODUCTS: THREE ISOFORMS, TWO SOLUBLE FORMS AND MEMBRANE-BOUND FORM EXIST DUE TO ALTERNATIVE SPLICING OF THE
LGRN1ACWFPRTFILSKGRDWLSVLVNGSSKHSAIRPFDQLFALHAIDQINPPLNVTAEI 249
                                                                                                                                                                                        DTEIKVNPPQDFEIVDPGYLGYLYLQWQPPLSLDHFKECTVEYELKYRNIGSETWKTIIT 86
                  -GQNIGCREP--YLEASDYKDFYICVNGSSENKPIRSSYETEQLQNIVKPLPPVYLTETR
                                                       TMTTEDNYSRLRSYQVSLHCTWLVGTDAPEDTQYFLYYRYGSWTE----
                                                                                                         ES---KCVTILHKGFSASVRTILQ---NDHSLLASSWASAELH-APPGSPGTSIVNLTCT 135
                                                                                                                                   KNLHYKDGFDLNKGIBAKIHTLLPWQCTNGSEVQSSWAETTYWISPQGIPETKVQDMDCV 146
                                                                                                                                                               DEKISLLPPVNETIKVTG-LAQVLLQWKPNPDQEQ-RNVNLEYQVKINAPKEDDYETRIT
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                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                            420
                                                                             ---YYNWQYLL-CSWKPGIGVLLDTNYNLFY----WYEGLDHALQCVDYIKAD 191
                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HETERCDIMER OF AN ALPHA AND A BETA CHAIN. COMMON TO THE IL-3, IL-5 AND GM-CSF RECEP
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                                                                                                                                                                                                                                                                                       POTENTIAL.

POTENTIAL.

NDE -> FSR (IN SOLUBLE ISOFORM S1)

MISSING (IN SOLUBLE ISOFORM S2).

N -> K (IN SOLUBLE ISOFORM S2).

MISSING (IN SOLUBLE ISOFORM S2).

MISSING (IN SOLUBLE ISOFORM S2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RECEPTOR FOR INTERLEUKIN-5.
                                                                                                                                                                                                                                    Score 310.5;
Pred. No. 3.6
                                                                                                                                                                                                                                                                                                                                                                                                  CYTOPLASMIC POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                     POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                         INTERLEUKIN-5
EXTRACELLULAR
                                                                                                                                                                                                                                                                                                                                                                                                                             POTENTIAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Noved. Usage by and for (See http://www.isb-sib
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Alternative splicing; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FALSE_NEG
                                                                                                                                                                                                                                    .6e-17;
                                                                                                                                                                                                                                                                                                                                                                                                               (POTENTIAL)
                                                                                                                                                                                                                                                 DB 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AND BASOPHILS F RECEPTORS.
                                                                                                                                                                                                                                                 Length 420;
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                                                       -ECQEYSKDT
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                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                     CARBOHYD
                                          CARBOHYD
                                                   CARBOHYD
                                                                                                                                                                                                 or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          009030;
                            CARBOHYD
                                                                                                                                                                   MGD; MGI:105052;
                                                                                                                                                                             EMBL; S80963; AAB50695.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HILTON D.J., ZHANG J.-G., METCALF D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-NOV-1997
                                                                                           DOMAIN
                                                                                                     DOMAIN
                                                                                                                          DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13RA-1) (INTERLEUKIN-13 BINDING PROTEIN)
IL13RA1 OR IL13RA OR IL13R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-1997 (Rel. 35, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
INTERLEUKIN-13 RECEPTOR ALPHA-1 CHAIN PRECURSOR
                                                                                                                TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    309
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      362 CKICHLWIKLFP 373
                                                                                                                                                                                                                                                                                   TESTIS, STOMACH, BRAIN, SKIN, AND COLON; BUT NOT SKELETAL MUSCLE SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN. SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
                                                                                                                                                                                                                                                                                                       SUBUNIT: INTERLEUKIN-13 RECEPTOR IS A COMPLEX OF IL4R-ALPHA, IL13R-ALPHA, AND POSSIBLY OTHER COMPONENTS (BY SIMILARITY). SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN. TISSUE SPECIFICITY: SPLEEN, LIVER, THYMUS, HEART, LUNG, KIDN TESTIS, STOMACH, BRAIN, SKIN, AND COLON; BUT NOT SKELETAL MU
                                                                                                                                                                                                                                          European Bioinformatics Institute.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RAAVSSMCREAGLWSEWS-QPIYVGNDEHKP--LREW----FVIVIMATICFILLILSLI
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96133964.
                                                                                                                                                                                                            requires a license agreement (See http://www.isb-sib.ch/announce/
IN ALLOWING ENHANCED IL-2 BINDING ACTIVITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                    IL13RA
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                                                                                                    340
364
424
                                                                                                                                                         Glycoprotein;
        POTENTIAL.
                             POTENTIAL.
                                                           BY SIMILARITY
                                                                      BY SIMILARITY
                                                                                IG-LIKE C2-TYPE POTENTIAL.
                                                                                                    CYTOPLASMIC (POTENTIAL)
                                                                                                               EXTRACELLULAR (POTENTIAL).
POTENTIAL.
                                       POTENTIAL.
                                                  POTENTIAL
                                                                                                                                    INTERLEUKIN-13
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                                                                                                                                               OTENTIAL
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                                                                                                                                                        Immunoglobulin
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                                                                                                                                   RECEPTOR ALPHA-1
                                                                                                                                                                                                                    Usage
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (IL-13R-ALPHA-1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mammalia;
Mus.
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RESULT 4
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Best Local !
                                                                                                                                                                                                                                                                                                                                                                                                                                                        P78552; 099656;
01-:0V-1997 (Rel. 35, Created)
01-:0V-1997 (Rel. 35, Last sequence update)
15-JJL-1999 (Rel. 38, Last annotation updat
15-JJL-1999 (Rel. 38, Last annotation updat
                                                MEDLINE;
                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens (Human).

Homo sapiens (Human).

Chordata;
receptor alpha
                                                                                                                                               JEANNIN P., SEQUANI S., ELSON G.,
                                                                                                                                                                                GAUCHAT J.F.M., SCHLAGENHAUF E.,
                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                             IL4R alpha of a functional IL FEBS Lett. 401:163-166(1997).
                                                                                                                                 Submitted
                                                                                                                                                                                                                                                              "Cloning of the human IL-13R alphal chain and reconstitution with the IL4R alpha of a functional IL-4/iL-13 receptor complex.";
                                                                                                                                                                                                                                                                                                   FERRARA P
                                                                                                                                                                                                                                                                                                                    MILOUX B
                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                    Eutheria;
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                                                                                                                                                                                                   CISSUE-B-CELL;
                                                                                                                                                                                                                                                                                                                                MEDLINE; 97165986
cDNA cloning and characterization eceptor alpha chain.";
                                EONARD W.J.;
                                                                                               EQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VEY-- - ELKYRNIGSETWKTIITKNLHYKDGFDLNKGIEAKIHTLLPWQCT-NGSEVQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LGELLVLLLWTATVGQVAAA-*-TEVQPPVTNLSVSVENLCTIIWTWSPPEGAS--PNCT
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                                                                                                                                                                                                                                                                                                                  ., LAURENT
                                                                                                                                                                                                                                                                                                                                                                                                  Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          424 AA;
                                              TAYEBI N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                P.,
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                                                                                                                                g
                                              OBIRI N.I.,
                                                                                                                                                                                                                                                                                                                BONNIN O., LUPKER J., CAPUT D., VITA N.,
                                                                                                                              the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ₩;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          70;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 298; DB Pred. No. 3.5e
                                                                                                                                                                                                                                                                                                                                                                                                                   Craniata; Vertebrata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          111E5963 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                  Hominidae;
                                                                                                                                                               FENG N.P., MC, NOTARANGELO
                                                PURI R.K., MODI W.S.,
             Or,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      427
             the human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 1;
.5e-16
                                                                                                                                                             MOSER R.,
               interleukin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (IL-13R-ALPHA-1) (IL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 424
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               13
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Best Local S
Matches 107
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EMBL; Y09328;
EMBL; U62858;
EMBL; U62858;
HSSP; P31785;
MIM; 300119;
                                                                                                                                                                                                                                                                                                                          CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    J. Biol. Chem. 271:29265-29270(1996).

11. FUNCTION: BINDS IL-13 WITH A LOW AFFINITY. TOGETHER WITH IL-4R-ALPHA CAN FORM A FUNCTIONAL RECEPTOR FOR IL-13. ALSO SERVES AS:
ALPERNATE ACCESSORY PROTEIN TO THE COMMON CYTOKINE RECEPTOR GAM
ALTERNATE ACCESSORY PROTEIN TO THE COMMON CYTOKINE RECEPTOR GAM
CHAIN FOR IL-4 SIGNALING, BUT CANNOT REPLACE THE FUNCTION OF
GAMMA-C IN ALLOWING ENHANCED IL-2 BINDING ACTIVITY.

11. SUBUNIT: INTERLEUKIN.13 RECEPTOR IS A COMPLEX OF IL4R-ALPHA,
                                                                                                                                                                                                                                                                                             CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TRANSMEM
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PFAM; PF00041; fn3; 1
184 CVDYIKADGONIGCREPYLEASD -- YKDEYICVNGSSENKPIRSSYFTFQLQNIVKPLPP 241
                              115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        eceptor;
                                                            125
                                                                                        83
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                                                                                                                                                10
                                                                                                                                                                            11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ILIN-ALPHA, AND POSSIBLY OTHER COMPONENTS.
SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
TISSUE SEBCIFICITY: UBJOULTOUS, HIGHEST LEVELS IN HEART, LIVER,
SKELETAL MUSCLE AND OVARY; LOWEST LEVELS IN BRAIN, LUNG AND
KIDNEY. ALSO FOUND IN B-CELLS, T-CELLS AND ENDOTHELIAL CELLS.
SIMILARITY: CONTAINS 1 IMMUNOCLOBULIN-LIKE C2-TYPE DOMAIN.
SIMILARITY: CONTAINS 1 FIBRONECTIN TYPE III-LIKE DOMAIN.
SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
                                                                                                                                                                           LYTELISTIFGCTSSSDTEIKVNPPQDFEIVDPGYLGYLYLQWQPPLSLDHFKECTVEY- 70
                           EKC--ISPPEGDPESAVTELQCIWHNLSYMKCSWLPGRNTSPDTNYTLYYWHRSLEKIHQ 172
                                             ETTYWIS-PQGIPETKVQDMDCVYYNWQYLLCSWKPGIGVLLDTNYNLFYWYEGLDHALQ 183
                                                                                    SHFGDKQDKKIAPETRRSI-----EVPLNERICLQVGS----QCSTNESEKPSILV 114
                                                                                                        ----ELKYRNIGSETWKTIITKNLHYKDGFDLNKGIEAKIHTLLPWQC-TNGSEVQSSWA 124
                                                                                                                                              LWALLLCAGGGGGGGGAAPTETQPPVTNLSVSVENLCTVIWTWNPPEGAS--SNCSLWYF 67
                                                                                                                                                                                                         107;
                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Transmembrane;
                                                                                                                                                                                                                                                                                                             37
105
138
157
157
235
293
329
3329
                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; CAA71669.1; -.
; CAA70508.1; -.
; AAB37127.1; -.
                                                                                                                                                                                                                                                                                 48759
                                                                                                                                                                                                                       14.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Glycoprotein; Immunoglobulin domain; Signal POTENTIAL.
                                                                                                                                                                                                                                                                               MW;
                                                                                                                                                                                                         63;
                                                                                                                                                                                                      Score 295.5;
Pred. No. 5.5e
53; Mismatches
                                                                                                                                                                                                                                                                                                                          POTENTIAL.
                                                                                                                                                                                                                                                                                              ရ <del>မ</del>
                                                                                                                                                                                                                                                                                                                                                                   POTENTIAL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                           POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IG-LIKE C2-TYPE DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INTERLEUKIN-13 RECEPTOR ALPHA-1 CHAIN
                                                                                                                                                                                                                                                                              -> I (IN REF. 3).
-> D (IN REF. 3).
88E33C57 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SIMILARITY.
                                                                                                                                                                                                      .5e-16;
ies 169;
                                                                                                                                                                                                                                   DB 1;
                                                                                                                                                                                                                                   Length 427;
                                                                                                                                                                                                        Indels
                                                                                                                                                                                                        73;
                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GAMMA
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DOMAIN OF DOMAIN

DOMAIN

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FIBRONECTIN TYPE-III.
FIBRONECTIN TYPE-III.
FIBRONECTIN TYPE-III.

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BY SIMILARITY.

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PPLR_CHICK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-JUN-1994 (Rel.
01-JUN-1994 (Rel.
15-JUL-1998 (Rel.
                                                                                                                                                                                                                                                                                              use by non-profit institutions as long as its content modified and this statement is not removed. Usage by an
                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                            -1: SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
-:- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
-:- SIMILARITY: CONTAINS 4 FIBRONECTIN TYPE III-LIKE DOMAINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Archosauria;
                                                                                                                                               PROSITE; PS00241; RECEPTOR_CYTOKINES_1; PROSITE; PS00340; RECEPTOR_CYTOKINES_2;
                                                                                                                                                                                 HSSP; P16471; 1BP3.
PFAM; PF00041; fn3;
                                                                                                                                                                                                                                   EMBL; D13154;
                                                                                                                                                                                                                                                                 or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Biochem. Biophys.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              the cDNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-WHITE LEGHORN; TISSUE-KIDNEY; MEDLINE; 93075121.
                                                   DOMAIN
                                                                TRANSMEM
                                                                                   DOMAIN
                                                                                                   CHAIN
                                                                                                                    SIGNAL
                                                                                                                                   Receptor;
                                                                                                                                                                                                                                                                                  entities requires a license agreement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TANAKA M., MAEDA K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Neognathae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 !- FUNCTION: THIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ANAKA M., MAEDA K., OKUBO T., NAKASHIMA
Double antenna structure of chicken proj
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              340 RNSTLYITMLLIVPVIVAGAIIVLLLYLKRLKIIIFPPIPDPGKIFKEMFGD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               340 TLLREWLPF------GFILILVIFVTGL--LLRKPNTYP-KMIPEFFCD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             242 --VYLTFTRESSCEIKLKWSIPLGPIPARCFDYEIEIREDDTT-----LVTATVENETY
                                                                                                                                                                                                                  JQ1655;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ERNVENTS---CFMVPGVLPDTLNTVRIRVKTNKLCYEDDKLWSNWSQEM----SIGKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C-ENIFREGQYFGCSFDLTKVKDSSFEQHSVQIMVKDNAGKIKPSFNIVPLTSRVKPDPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TLKTTNETRQLCFVV-------RSKVNIYC-SDDGIWSEWSDKQCWEGEDLSKK
                                                                                                                                 Transmembrane; Glycoprotein; Signal; Repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gallifcrmes; Phasianidae;
                                                                                                                                                                                                                JQ1655.
                                                                                                                                                                                                                                   BAA02439.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  29, Created)
29, Last sequence update)
36, Last annotation update)
R PRECURSOR (PRL-R) (CPRLP).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Res.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SI
                                                                                   23
831
438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A RECEPTOR FOR THE ANTERIOR PITUITARY HORMONE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Commun.
                                                 CYTOPLASMIC
                                                                  POTENTIAL
                                                                                 EXTRACELLULAR (POTENTIAL)
                                                                                                 PROLACTIN RECEPTOR
                                                                                                                    POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               prolactin receptor deduced
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Phasianinae; Gallus.
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                                                 (POTENTIAL).
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Best Local S
Matches 103
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CARBOHYD
CARBOHYD
SEQUENCE
                                                                                                                                                                                   receptor.
                                                                                                                                                                                                                                                                                                                                                         01-MAY-1991 (Rel. 18, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                              P21183;
01-MAY-1991 (Rel. 18, Created)
                                                                                                                                                                                                                                                                                                                   Mus musculus (Mouse)
                        This SWISS-PROT entry is copyright. It is produced through a c
between the Swiss Institute of Bioinformatics and the EMBL
                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa;
Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                 INTERLEUKIN-5 RECEPTOR ALPHA CHAIN IL5RA OR IL5R.
                                                                                                                                                                                                                                                   MEDLINE;
                                                                                                                                                                                                            Molecular cloning and expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       347
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                                                                                                                                                                                                                             AKATSU K.;
                                                                                                                                                                                                                                                    EQUENCE FROM N.A. EDLINE; 91092260.
                                                                                                                                                                                                                                                                                                                                                                                                               L5R_MOUSE
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European Bioinformatics Institute. The by non-profit institutions as long
                                                                                                     SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA CHAIN. THE CHAIN IS COMMON TO THE IL-5, IL-5 AND GM-CEF RECEPTORS SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
TISSUE SPECIFICITY: EXPRESSED ON EOSINOPHILS AND BASOP!
                                                                SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS SIMILARITY: TO IL-13 RECEPTOR ALPHA-2 CHAIN.
                                                                                                                                                         FUNCTION: THIS IS BINDS TO IL-5.
                                                                                          ON B-CELLS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PEGEI--LILVIEVTGLLLRKPNTYPKMIP 374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LPPVYLTFTRESSCEIK----LKWS-IPLGPIPARCFDYEIEIR---EDDTTLVTATVEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DASSNHLYHYELRIKPEEKEEWETI---SVGVQTQCKINR-LNAGMRYVVQVRCTLDPGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VLGVLSSLICLIMSWTMVLKGYRMITFMLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QTQYKMFSLNPGKKYI-----IQIHCKPDHHGSWSEWSSENYIQIPNDFRVKDMI-VWI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ET-YTLKTTNETROLCFVVRSKVNIYCSDD--GIWSEWSDKQCWE-GEDLSKKTLLRFWL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DPPVNVTLELKKPINRKPYLVLTWSPFPLADVRSGWLTLEYELRLKPEEGEEWETIFVGQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EQYYECPDY-RTAGPN-SCYFDKKHTSFWTIYNITVRATNEMGSNSSDPHYVDVTYIVQP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WSEWSSERHILIPSGQSPPEKPTIIKCRSPEKETFTCWWKPGLDGGHPTNYTLLYSKEGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QSSWAETTYWISPQG-IPETKYQDMDCVYYNWQYLLCSWKPGIGVLLDTNYNLFYWYEGL 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TTFGCTSSSDTEIKVN--PPQDFE---IVDPG-----YLGYLYLQWQPPLSL 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DHALQCVDYIKADGQNIGCRFPYLEASDYKDFYICVNGSSENKPIRSSYFTFQLQNIVKP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      103;
                                                                                                                                                                9:4367-4374(1990).
CTION: THIS IS THE RECEPTOR FOR INTERLEUKIN-5. THE ALPHA
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                                                                                                                                                                                                                                        ., TOMINAGA
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831 AA;
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315
335
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                                                                                                                                                                                                                                                                                          Chordata; Craniata; Vertebrata; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                       Chordata;
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                                                                                                                                                                                                                                      MITA S.,
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POTENTIAL.
8977BF07
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Pred. No. 4.2e-13;
                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
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                                                                                                                                                                                                             of the murine interleukin-5
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Mus.
            restrictions
                           a collaboration
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RESILE 7

PALK\_MELGA STANDARD; PRT; 8

II PALK\_MELGA STANDARD; PRT; 8

IC Q91094; Q91091; Q91092;

D2 31-NOV-1997 (Rel. 35, Created)
D7 01-NOV-1997 (Rel. 35, Last sequence up
D7 15-JUL-1999 (Rel. 38, Last annotation
DF PROLACTIN RECEPTOR PRECURSOR (PPL-R) (

update) n update) (TPRLR).

831

AA

8888

Neognathae;

Calliformes;

Meleagrididae;

Meleagris

Archosauria;

Aves;

PRLR. Meleagris gallopavo

Meleagris gallopavo (Common turkey). Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;

SEQUENCE FROM N.A. TISSUE-KIDNEY: MEDLINE; 57057891.

57057891.

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350
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VCHLWTRLFP
                          KPNTYPKMIP 374
                                                                                                                                                              TEINSKGEEQLAVUINGSSKRAAIKPEDQLESPLAIDQVNPPRNVTVEIESN-SLYIQWE
                                                                                                                                                                                                                                                                                               GEDLNKGIEAKIHTLLPWQCTNGSEVQSSWAETTYWISPQGIPETKVQDMDCVYYN----
                                                                                                                                                                                                                                                                                                                           PPVNETIKATG-LAQVLLHWDPNPDQEQ-RHVDLEYHVKINAPQEDEYDTRKTES---KC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MGI:96558
                                                                              RSKVNIYCSDDGIWSEWSDKQCWEGEDLSKKTLLRFW----LPFGFILILVIFVTGLLLR
                                                                                                         KPLSAFPDHCFNYELKIYNTKNGHIQKEKLIANKFISKIDDVSTYSIQ------V
                                                                                                                                  IFLGPIFARCEDYEIEIREDD# ----
                                                                                                                                                                                    -YLEASDYKDFYICVNGSSENKPIRSSYFTFQLQNIVKPLPPVYLTFTRESSCEIKLKWS
                                                                                                                                                                                                                  HTHLRP QVSLRCTWLVGKDAPEDTQYFLYYRFGVLTE - - KCQEYSRDALNRNTACWFPR
                                                                                                                                                                                                                                           -----WQY-LLCSWKPGIGVLLDTNYNLFYWYEGLDHALQCVDYIK-ADGQNIGCRFP-
                                                     RAAVSSPCRMPGRWGEWS-QPIYVGKE--RKSLVE-WHLIVLPTAACEVLLIE--SLICR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               D90205; BAA14231.1;
                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PS00241; RECEPTOR_CYTOKINES_1; FALSE_NEG PS00340; RECEPTOR_CYTOKINES_2; 1. ; Transmembrane; Glycoprotein; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Transmembrane;
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369
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24.6%;
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BY SIMILARITY.
POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                           Score 247; DB 1;
Pred. No. 3.2e-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INTERLEUKIN-5 RECEPTOR ALPHA CHAIN. EXTRACELLULAR (POTENTIAL). PCTENTIAL CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                               POTENTIAL
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                                                                                                                                  -----TTLVTATVENETYTLKTTNETRQLCFVV
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                                                                                                                                                                                                                                                                                                                                                                                                        Length 415
                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                58;
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                                                                              364
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PITTS G.R., YOU S.K., FOSTER D.N., EL HALAWANI M.E.; Submitted (MAR-1995) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: THIS IS A RECEPTOR FOR THE ANTERIOR PITUITARY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PS00241; RECEPTOR_CYTOKINES_1; 2.
PROSITE; PS00340; RECEPTOR_CYTOKINES_2; 2.
Receptor; Transmembrane; Glycoprotein; Signal; Repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; L76587; AAB01544.1; -.
EMBL; U22947; AAA75038.1; -.
EMBL; U22924; AAA75039.1; -.
HSSP; P16471; 1BP3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a between the Swiss Institute of Bioinformatics and the EMBI the European Bioinformatics Institute. There are no restrict
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZHOU J.F., ZADWORNY D., GUEMENE D., KUHNLEIN U.;
"Molecular cloning, tissue distribution, and expression of the prolactin receptor during various reproductive states in Meleagris gallopavo.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 82-121 AND 473-522 FROM
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              179
                                        213
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SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
SIMILARITY: CONTAINS 4 FIBRONECTIN TYPE III-LIKE DOMAINS.
DHALQCVDYIKADGQNIGCREPYLEASDYKDEYICVNGSSENKPIRSSYETFQLQNIVKP
                                                                                                                                                                                TTFGCTSSSDTEIKVN--PPQDFE---IVDPG-----YLGYLYLQWQPPLSL 59
                                        WSEWSSERRILISGGLSPPEKPTITKCRSPEKETFTCWWKPGLDGGHPTNYTLLYSKEGE
                                                        QSSW-AETTYWISPQGIPETKVQDMDCVYYNWQYLLCSWKPGIGVLLDTNYNLFYWYEGL 178
                                                                                              DASSNHLYHYELRLKPEEKEEWETV----PVGVQTQCKINR-LNAGMRYVVQVRCMLDPGE
                                                                                                                       DHFKECTVEYELKYRNIGSETWKTIITKNLHYKDGFDLNKGIEAKIHTLLPWQCTNGSEV 119
                                                                                                                                                    TTYNITYTATNEIGSNSSDPQYVDVTSIVQPGSPVNLTLETQRYANIMYLWAKWSPPLLA 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Reprod. 55:1081-1090(1996).
                                                                                                                                                                                                            1 Similarity 26.:
97; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              439
460
25
123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      fn3; 4.
                                                                                                                                                                                                                                                                                94394 MW;
                                                                                                                                                                                                                         11.3%;
26.1%;
                                                                                                                                                                                                            53;
                                                                                                                                                                                                          Score 238; DB 1; 1
Pred. No. 3.7e-11;
53; Mismatches 178;
                                                                                                                                                                                                                                                                                                                                     POTENTIAL.
POTENTIAL.
POTENTIAL.
                                                                                                                                                                                                                                                                               POTENTIAL. FB715C98 CRC32;
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FIBRONECTIN TYPE-III.
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PROLACTIN RECEPTOR
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                                                                                                                                                                                                                                      Length 831;
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NEGLINE; 94090
NOGUCHI M., NZ
LEONARD W.J.;
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01-JUL-1993 (Rel. 26, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
CYTOKINE RECEPTOR COMMON GAMMA CHAIN PRECURSOR (GAMMA-C) (INTERLEUKIN-
2 RECEPTOR GAMMA CHAIN) (IL-2R GAMMA CHAIN) (P64) (CD132 ANTIGEN)
                                                                                                                                                                                         ARAI K.-I., SUGAMURA K.;
"Sharing of the interleukin-2 (IL-2) receptor receptors for IL-2 and IL-4.";
Science 262:1874-1877(1993)
                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A., AND VARIANTS ASP-114 AND MEDLINE; 94004847.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A., AND PARTIAL SEQUENCE MEDLINE; 92335883.
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Homo sapiens (Human).
Motazoa; Chordata;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NOGUCHI M., ADELSTEIN S., CAO X., LEONARD W.J.; "Characterization of the human interleukin-2 receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE; 93293887
                                                                                                                                                                                                                                                                                                                      "The interleukin-2 receptor gamma chain maps to xq13.1 in X-linked severe combined immunodeficiency, SCIDX1.", Hum. Mol. Genet. 2:1099-1104(1993).
                                                                                                                                                                                                                                                                                                                                                       WILLARD H., HENTHORN P.S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eutheria; Primates;
                           IDENTIFICATION AS A IL-7R SUBUNIT.
MEDLINE; 94090316.
                                                                        Science
                                                                                                                                           RUSSELL S.M.,
                                                                                                                                                              MEDLINE;
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                                                                       interleukin-4 receptor.";
Science 262:1880-1883(1993).
                                                                                                                                 LELAND P
                                                                                                                                                           MEDLINE; 94090317.
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                                                                                         interleukin-2 receptor gamma chain: a
iterleukin-4 receptor.":
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               RUSSELL S.M.,
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                ZIEGLER
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                S.F.,
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immunodeficiency in the IL-2R gamma conformation polymorphism analysis.";
Hum. Genet. 96:427-432(1995).
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KONNO T., MAEDA M., UCHIYAMA T.,
KIMPairment of ligand binding and
"Impairment of ligand binding and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Detection of three nonsense mutations the interleukin-2 receptor gamma chain differently affect the mRNA processing. Genomics 21:291-293(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Interleukin-2 (IL-2) receptor gamma chain mutations in X-linked severe combined immunodeficiency disease result in the loss of high-affinity IL-2 receptor binding.";
Eur. J. Immunol. 24:475-479(1994).
                                                                gamma-chain mutation causing X-linked
                                                                                                                                                                                                                                                                                                                                                                      chromosome-linked severe
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                                                                                                                                                                                                       CLARK P.A., LESTER T.,
                                                                                                                                                                                                                   WARIANT XSCID SER-183. MEDLINE; 96013903.
                                                                                                                                                                                                                                             "Two mutational hotspots in the interleukin-2 receptor gamma chain gene causing human X-1inked severe combined immunodeficiency."; hm. J. Hum. Genet. 57:564-571(1995).
                                                                                                                                                                                                                                                                                             MEDLINE; 95397841.
PEPPER A.E., BUCKLEY R.H.,
                                                                                                                                                                                                                                                                                                                                                            cells.
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     VARIANT XSCID GLN-271 MEDLINE; 95190013.
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                                        .mmunodeficiency.
J. Clin. Invest.
                                                                              'Female germ line mosaicism as
                                                                                         PUCK J.M., PEPPER A.E.,
                                                                                                                   VARIANT XSCID
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94375038.
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                                                                                                                  GLN-HIS-TRP INS-237.
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                                          95:895-899(1995)
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PROBABLY ALSO THE IL-13 RECEPTORS.
-I- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN
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MEDLINE; 97042245.
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Genet. 99:677-680(1997).
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                           PS00241; RECEPTOR_CYTOKINES_1; PS00340; RECEPTOR_CYTOKINES_2; Transmembrane; Glycoprotein; ;
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sion of the genetic defect in T cells.";
335:1563-1567(1996).
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H., FISCHER
                                                                                                                                                                                                                                                                                                                                                                                            its content
                               Disease mutation;
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PRLR_COLLI
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TRANSMEM
                                                                                                                                                                                                                                                                                                                  the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed. entitles requires a license agreement (See or send an email to license@isb-sib.ch).
                  DOMAIN
                                                                                                                                                              Receptor;
                                                                                                                                                                                                                                                              EMBL; U07694;
HSSP; P16471;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q90374;
01-NOV-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Columba livia (Domestic pigeon).
Eukaryota; Metazoa; Chordata; Craniata;
Neognathae; Columbiformes; Columbidae; (
                                                                                                                                         CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  endocrinology 135:269-276(1994).
-!- FUNCTION: THIS IS A RECEPTOR
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                                                                                                                                                                                                    PROSITE;
                                                                                                                                                                                                                        PROSITE;
                                                                                                                                                                                                                                             PFAM; PF00041;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
SIMILARITY: CONTAINS 4 FIBRONECTIN TYPE III-LIKE DOMAINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROLACTIN
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RECEPTOR_CYTOKINES_2; 2.
mbrane; Glycoprotein; Signal; Repeat.
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3; Mismatches
                                                        CYTOPLASMIC (POTENTIAL) FIBRONECTIN TYPE-III.
  FIBRONECTIN
                FIBRONECTIN
                                                                                               EXTRACELLULAR (POTENTIAL).
POTENTIAL.
                                                                                                                                         PROLACTIN RECEPTOR
                                                                                                                                                              POTENTIAL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3.5e-10;
ches 121;
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                  TYPE-III.
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TYPE-III
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RESULT 10
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Best Local: S
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01-FEB-1994 (Rel. 2
15-DEC-1998 (Rel. 3
CYTOKINE RECEPTOR C
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SEQUENCE
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                       KUMAKI S.; KONDO M., TAKESH "Cloning of the mouse inter demonstration of functional
                                                              SEQUENCE FROM N.A. MEDLINE; 93277575.
                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                    P34902;
  Biochem.
           receptors
                                                                                                                            Mus musculus (Mouse).
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                                                                                                                                                       (INTERLEUKIN-2 RECEPTOR
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                                                                                                                                                                                                                                                                                                                        KKTLLRFWLPFGFILILVIFV
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                                                                                                                                                                                                                                                                                                                                                                                                 VTYIVQTOPPVNVTLELKKTVNRKPYLVLTWSPPPLADVRSGWLTLDYELRLKPEEA---
                                                                                                                                                                                                                                                                                                                                                                                                                         LQNIVKPLPPYYLTETRESSCEIK----LKWS-IPLGPIPA--RCFDYEIEIREDDTTLV
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                                                                                                                                                                                                                                                                                                                                                ----EEWETIFVGQQTHYKMFSLNPGKKYIVQIHCKPDHHGSWSEWSLEKYLQIPTDFR
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 Biophys.
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100
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263
3164
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1. 28, Last sequence update;
1. 37, Last annotation update;
OR COMMON GAMMA CHAIN PRECURSOR ((RECEPTOR GAMMA CHAIN) (IL-2R GAMM
                                                                                                                                                                                                                                  STANDARD;
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Res.
                                                 TAKESHITA
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                       TAKESHITA T., ASAO
interleukin 2 rece
tional differences
 Commun.
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Pred. No. 1.7e-09;
3; Mismatches 174;
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5EFADD51 CRC32;
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193:356-363(1993)
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          369
                                      H., NAKAMURA M.,
eptor gamma chain:
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GAMMA CHAIN) (P64).
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                                                                                                                  Mammalia
                           mouse
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STRAIN-CBA/CA;
MEDLINE; 93391374.
CAO X., KOZAK C.A.,

LIU

Y.J.,

NOGUCHI M.,

O'CONNELL E., LEONARD W.J.;

SEQUENCE FROM N.A.

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EMBL; D13565; EMBL; C120048; A EMBL; C120048; A EMBL; S75844; A EMBL; S75847; A EMBL; S75848; A EMBL; S75848; A EMBL; S75849; A EMBL; S75849; A EMBL; S75851; A EMBL; 
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                                      TRANSMEM
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DOMAIN
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"The murine interleukin-2 receptor gamma chain gene: chromosomal localization and expression in the adult Eur. J. Immunol. 24:3014-3018(1994).
                                                                                              CHAIN
DOMAIN
                                                                                                                                    Receptor;
SIGNAL
                                                                                                                                                                                                                                                                     PIR; JN0592; PIR; JN0775;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; D13821; EMBL; U21795;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             J. Neurooncol. 26:231-239(1995).
-I- FUNCTION: COMMON SUBUNIT FOR THE RECEPTORS FOR A VARIETY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IL-2R gamma chain
Proc. Natl. Acad.
                                                                                                                                                                                                                                                   HSSP; P31785;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   or send an email to license@isb-sib.ch).
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DOUGHERTY G.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-B6.
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                                                                                                                                                                       PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      European Bioinformatics Institute. The by non-profit institutions as long
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUBJUNT: THE GAMMA CHAIN IS COMMON TO THE IL-2 PROBABLY ALSO THE IL-13 RECEPTORS.
SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     adhesion protein CD44
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                                                                                                                                                                                                             MGI:96551; IL2RG. PF00041; fn3; 1.
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5; JN0775.
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23
264
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102
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AAB32904.1;
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Sci. U.S.A. 90:8464-8468(1993)
                                                                                                                                                                       RECEPTOR_CYTOKINES_1; 1
RECEPTOR_CYTOKINES_2; F.
369
263
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369
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the cDNA e
                                                                                                                                                                     CYTOKINES_2; FALSE_NEG
POTENTIAL.
                                  CYTOPLASMIC
FIBRONECTIN
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                                                                                              EXTRACELLULAR (POTENTIAL)
                                                                                                                CYTOKINE RECEPTOR COMMON GAMMA CHAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DOUGHERTY S.T.,
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                                                                                                                                                     Signal.
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                                      TYPE-III
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CARBOHYD
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01-FEB-1995 (Rel. 31, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
CYTOKINE RECEPTOR COMMON GAMMA CHAIN PRECURSOR (GAMMA-C)
(INTERLEUKIN-2 RECEPTOR GAMMA CHAIN) (IL-2R GAMMA CHAIN) (P64).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CARBOHYD
CARBOHYD
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                                       between the Swiss Institute of Bicinf
the European Bicinformatics Institute.
                                                                    This
                                                                                                                                                           INTERLEGKINS.
-!- SITUANIT: THE GAMMA CHAIN IS COMMON FROBLEM, ALSO THE IL-13 RECEPTORS.
                                                                                                                                                                                                                    Genomics 23:69-74(1994)
                                                                                                                                                                                                                                             severe combined
                                                                                                                                                                                                                                                                                                                                                      Canis familiaris (Dog).
Canis familiaris (Dog).
Craniata; Vertebrata;
Craniata; Vertebrata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                    -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN
-!- DISEASE: DEFECTS IN IL2RG ARE THE CAUSE OF A
                                                                                                                                                                                                       "!- FUNCTION:
                                                                                                                                                                                                                                disease.
                                                                                                                                                                                                                                                                                                  MEDLINE;
                                                                                                                                                                                                                                                                      ELSBURG P.J.;
                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                          ^{\prime}IL-2R gamma gene microdeletion demonstrates that canine x-linked
                                                                                                                                                                                                                                                                                                                ISSUE-SPLEEN
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                                                                                       SEVERE COMBINED IMMUNODEFICIENCY.
SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
SIMILARITY: CONTAINS 1 FIBRONECTIN TYPE III-LIKE DOMAIN.
                                                   SWIJS-PROT entry is copyright. It is produced through a collaboration econ the Swiss Institute of Bioinformatics and the EMBL outstation -
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67: Conser
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                                                                                                                                                                                                                                             immunodeficiency is
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                             institutions as long
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 agreement
              is not removed
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Pred. No. 1.3e-09;
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                                     There are no
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CRC32;
                             as its content
. Usage by and for commercial http://www.isb-sib.ch/announce,
                                                                                                                                                                                                                                                                                   PUCK J.M., PATTERSON D.F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  116;
                                                                                                                                     CANINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length
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                                        restrictions
               and for
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           in no way
commercial
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RESULT
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Best Local Similarity
Matches 69; Conser
                                                                                                                                                                                                                                                                                                                                   ULT 12
B_MOUSE STANDARD
P26954;
01-0CT 1993 (Rel. 27, C.
01-0CT 1993 (Rel. 27, L.
15-JUL-1999 (Rel. 38, L.
                                               SEQUENCE FROM N.A.
MEDLINE; 90117145.
ITCH N.; VONEHARA S., SCHREURS J., GORMAN D.M., MARUYAMA K
YAHARA I., ARAI K., MIYAJIMA A.;
"Cloning of an interleukin-3 receptor gene: a member of a
receptor gene family.";
Science 247:324-327(1990).
                                                                                                                                                                                                                                                                             15-JUL-1999 (Rel. 27, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
1NTERLEUKIN-3 RECEPTOR CLASS II BETA CHAIN PRECURSOR.
AIZCA OR ILJRE OR ILJR.
Mus musculne 'Ve----
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                                                                                                                                                                                                                                                                      Mus musculus (Mouse)
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PROSITE; PS00340; RECEPTOR_CYTOKINES_2; FALSE_NEG
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    FUNCTION: IN MOUSE THERE ARE TWO CLASSES OF HIGH-AFFINITY IL-3 RECEPTORS. ONE CONTAINS THIS IL-3-SPECIFIC BETA CHAIN AND THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NKPIRSSYFTFQLQNIVKPLPPVYLIFTRESSCEIKLKWSIPLGPIPARCFDYEIEIRED
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Pred. No. 3e-09;
18; Mismatches 108
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FIBRONECTIN TYPE-III.
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                                                                                                                                 GORMAN D.M., MARUYAMA K., ISHII A.,
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PROSITE; PS00340; RECEPTOR_CYTOKINES_2; 1.
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or send an email to license@isb-sib.ch).
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-!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
-!- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS
                                                                                                                                                                                                                                        308 VRSK-VNIYCSDDGIWSEWSDKOCWEGEDLSKKTLLRFWLPFGFILILVIFVTGLLL
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                                                                                                                                                                                                   415 VRVKPISDY ---DGIWSEWSNEYTWT-TDWVMPTL---WI----VLILVFLIFTLLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  139 PPKDIHISPSG--DHFLLEWSVSLGDSQVSWLSSKDIEFEVAYKRL-QDSWED--ASSLH
                                                                                                                                                                                                                                                                              358 YSLHWETQKIP---KYIDHTFQVQYKKKSESWKDSKTENLGRVNSMDLPQLEPDTSYCAR 414
                                                                                                                                                                                                                                                                                                                       254 IKLKWSIPLGPIPARCFD--YEIEIREDDTTLVTATVEN----ETYTLKTTNETRQLCFV 307
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                                                                                                                                                                                                                                                                                                                                                                                                -GCRFPYLEASDYKDFYICVNGSSENKPIRSSYFTFQLQNIVKPLPPVY-LTFTRESSCE 253
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997 (Rel. 35; Created)
997 (Rel. 35, Last sequence update)
998 (Rel. 35, Last annotation update)
RECEPTOR COMMON GAMMA CHAIN PRECURSOR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 195; DB 1; I
Pred. No. 8.8e-08;
9; Mismatches 150;
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Best Local :
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CARBOHYD
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gamma gene.";
DNA Cell Biol. 15:453-459(1996):
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoldea; Bovidae;
                                                                                                                                                                                                                                                                                                                                                                                                                               TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; U33748; AAB07812.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (INTERLEUKIN-2 RECEPTOR GAMMA CHAIN) (IL-2R GAMMA CHAIN) (P64).
IL2RG.
                                                                                                                                                                                                                                                                                                                               CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                     DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                  NIAMOC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Cloning and chromosomal mapping
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OO J., STONE R.T.,
                                                       169
                                                                                                           111
                                                                                                                                                                                           135 IPETKVQDMDCVYYNWQYLLCSW-----KPGIGVLLDTNYNLFYWY---EGLDHALQCV 185
226 YTFRVRSRYNPLCGSAQHWSDWSYPIHW-GSNTSKENIENPENPSLFALEAVLIPLG 281
                            304
                                                                                                                                   186 DYIKADGONIGCRFPYLEASDYKDFYICVNGSSENKPIRSSYFTFOLONIVKPLPPVYLF 245
                                                                                                                                                                 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
SIMILARITY: CONTAINS 1 FIBRONECTIN TYPE III-LIKE DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FUNCTION: COMMON SUBUNIT FOR THE RECEPTORS FOR A VARIETY OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUBUNIT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INTERLEUKINS.
SUBUNIT: THE GAMMA CHAIN IS COMMON TO THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROBABLY ALSO THE IL-13 RECEPTORS
                                                    LRNLSEFQLELSWS----NRYLDHCLEHLVQYRSDRDRSWTEQSVDHRHSFSLPSVDAQKL
                                                                                                         HYLFSEGITSGCWFGKKEIRLYETFVVQLQDPREHR--KQPKQMLKLQDLVIPWAPENLT
                                                                                                                                                               LPLPKVQ---CFVFNVEYMNCTWNSSSEPQP-----NNLTLHYGYRNFNGDDKLQECG 110
                         LCFVVRSKVNIYCSDDGIWSEWSDKQCWEGEDLSKKTLLRFWLPFGFILILVIFVTG 360
                                                                              FTRESSCEIKLKWSIPLGPIPARCFDYEIEIRED-DTTLVTATVEN-ETYTLKTTNETRQ 303
                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           non-profit institutions we are by and to whence and this statement is not removed. Usage by and to whence and this statement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PS00241; RECEPTOR_CYTOKINES_1; PS00340; RECEPTOR_CYTOKINES_2;
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                                                                                                                                                                                                                    Conservative
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                                                                                                                                                                                                                                  9.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Glycoprotein;
                                                                                                                                                                                                                                                                                         WW;
                                                                                                                                                                                                                    42;
                                                                                                                                                                                                                                  Score 189.5;
Pred. No. 8.0
                                                                                                                                                                                                                                                                                                                                           POTENTIAL.
                                                                                                                                                                                                                                                                                                      POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                 CYTOPLASMIC FIBRONECTIN
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FALSE_NEG
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TYPE-III.
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                                                                                                                                                                                                                                            Length 379;
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-I SUBJUTT: HETERODIMER OF AN LILPA AND A BETA CHAIN. THE BETAGUST: HETERODIMER OF AN LILPA AND A BETA CHAIN. THE BETAGUST IS COMMON TO THE II-5 AND GM-CSF RECEPTORS.

-I- SUBJECTIVIAR LOCATION: TYPE I MEMBRANE PROTEIN.

-I- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
-I- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
-I- DATABASE: NAME-PROW; NOTE-CD guide CDw131 entry;
FWW-"http://www.ncbi.nlm.nih.gov/prow/cd/cdw131.htm".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CYRB_HUMAN
P32927;
                                                                                                                                                                                                                                              CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                         TRANSMEM
DOMAIN
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                                                                                                                                                                                                                           SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      the European Bioinformatics Institute. These by non-profit institutions as long
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (FEB-1991) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: HIGH AFFINITY RECEPTOR FOR INTERLEUKIN-3,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        granulocyte-macrophage colony-stimulating factor (GM-CSF): reconstitution of a high-affinity GM-CSF receptor."; Proc Natl. Acad. Sci. U.S.A. 87:9655-9659(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CSF2PB OR IJ.5RB OR IL3RB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ol-NOV-1997 (Ref. 35, Last annotation update)
CYTOKINE RECEPTOR COMMON BETA CHAIN PRECURSOR
                                                                                                                                                                                                                                                                                        CARBOHYD
                                                                                                                                                                                                                                                                                                           DISULFID
                                                                                                                                                                                                                                                                                                                                DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; M59941; AAA18171.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              entities requires a
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MEDLINE; 91088571
HAYASHID' K. KITAMURA T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens (Human)
Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-FEB-1995 (Rel. 01-NOV-1997 (Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REVISION TO 454.
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                                        97 VIPCQSFVVTDVDYFSFQPDRPLGTRLTVTLTQHVQPPEPRDLQISTDQDHFLLTWSVAL 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            138981;
                                                                                  VNPPQDFEIVDPGYLGY---
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                                                                                                                                           Similarity
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                                                                                                                          Conservative
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97335
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                                                                                                                                                                                                                                                                                                                                                                                                                                 897
443
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                                                                                                                                           8.5%;
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Last annotation updat
                                                                                                                                                                                                                           WW;
                                                                                                                        57;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             _CYTOKINES_2;
                                                                                                                      Pred. No. 1.76
7; Mismatches
                                                                                                                                                          Score 178.5;
                                                                                                                                                                                                                                                POTENTIAL
                                                                                                                                                                                                                                                                                                                                               CYTOPLASMIC (POTENTIAL). FIBRONECTIN TYPE-III. FIBRONECTIN TYPE-III.
                                                                                                                                                                                                                                                                                                         BY SIMILARITY.
BY SIMILARITY.
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                                                                                -LYLQWQPP----
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                                                                                                                                                              Length 897;
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                                                                                                  PROSITE;
                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                   TRANSMEM
                                                                                                                                                                                                                               use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                  receptor gene family.";

Proc. Natl. Acad. Sci. U.S.A. 87:5459-5463(1990).

Proc. Natl. Acad. Sci. U.S.A. 87:5459-5463(1990).

Proc. Natl. Acad. Sci. U.S.A. 87:5459-5463(1990).

INT. FUNCTION: HIGH AFFINITY RECEPTOR FOR INTERLEUKIN-3, INT.

AND GRANULCYTE-MACROPHAGE COLONY-STIMULATING FACTOR.

SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA CHAIN. THE SUBUNIT: IS COMMON TO THE IL-3, IL-5 AND GM-CSF RECEPTORS.

CHAIN IS COMMON TO THE IL-3, IL-5 AND GM-CSF RECEPTORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GORMAN D.M., ITOH N., KITAMURA T
YAHARA I., ARAI K., MIYAJIMA A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. MEDLINE; 90319131.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota, Metazoa; Chordata; Craniata; Vertebrata;
Eukheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-OCT-1993 (Rel. 27, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
CYTOKINE RECEPTOR COMMON BETA CHAIN PRECURSOR
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                                  DOMAIN
                                                   CHAIN
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                                                                                 leceptor;
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                                                                                                                                                 A35782; A35
MGI:96554;
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PS00340;
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                                                                                                RECEPTOR_CYTOKINES_1; 1. RECEPTOR_CYTOKINES_2; 1.
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                                  CYTOKINE RECEPTOR EXTRACELLULAR (PO
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K-TDWVMPTL---WI----VLILVFLILTLLL 461
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                       EGEDLSKKTLLRFWLPFGFILILVIFVTGLLL
                                              VQYKKKSDSWEDSKTENLDRAHSMDLSQLEPDTSYCARVRVKPISNYDGIWSKWSEEYTW
                                                                     IEIREDDTTLYTATVEN--ETYTLKTTNETROLCFVVRSKVNIYCSDDGIWSEWSDKOCW
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FIBRONECTIN TYPE-III.
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BY SIMILARITY.
POTENTIAL.
POTENTIAL.
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Pred. No. 4.3e-06;
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Search completed: January 20, 2000, 06:19:55 Job time: 92 sec

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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Q14431 homo sapien
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Q16564 homo sapien
Q18985 cervus elap
P97378 mus musculu
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EMBL: U65747; AAC33240.1; -.
-EMQUENCE 383 AA; 44483 MW; 5
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"The murine IL-13 receptor alpha 2: molecular cloning, chiracterization, and comparison with murine IL-13 rec
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DONALDSON D.D., WHITTERS M.J., FITZ L., NEBEN T.Y.,
HENDERSON S.L., O'HARA R.M. JR., BEIER D.R., TURNER
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24: PYYLIFT RESSCEIKLKWSIPLGPIPARCFDYEIEIREDDTTLYTATVENETYTLKTTNE | : | : | : | : | : | : | : | : | | : | : | : | : | : | : | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : 
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Q92913 homo sapien
Q92913 oryctolagus
Q10466 homo sapien
O57520 xenopus lae
Q46600 bos taurus
Q89600 vesicular s
Q89604 vesicular s
Q89604 vesicular s
Q81210 caenorhabdi
Q27950 bos indicus
Q0227 homo sapien
Q63257 rattus norv
Q88999 vesicular s
Q8206 bos taurus
Q07784 gallus gall
Q62960 rattus norv
Q70535 rattus norv
Q70535 rattus norv
Q70535 rattus norv
Q70534 drosophila
Q62960 rattus norv
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SEQUENCE
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MEDLINE; 92121815.
MURATA Y., TAKAKI S., MIGITA M., KIKUCHI Y., TO
"Molecular cloning and expression of the human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
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UNTERLEUKIN-5 RECEPTOR P
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3L; X61176; CAA43483.1; -.
  CKICHLWIKLFP
                                                LRKPNTYPKMIP
                                                                                                                                            RSKVNIYCSDDGIWSEWSDKQCWEGEDLSKKTLLRFWLPFGFILIL -----VIFVTGLL 362
                                                                                                                                                                                                                                         ESSCEIKLKWSIPLGPIPARCFDYEIEIREDDTTLVTATVENETYTLKTTNETRQLCFVV
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                                                                                            RAAVSSMCREAGLWSEWS-QPIYVGNDEHKP--LREW----FVIVIMATICFILLILSLI
                                                                                                                                                                                             EGT-RLSIQWEKPVSAFPIHCFDYEVKIHNTRNGYLQIEKLMTNAFISIIDDLSKYDVQV
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Pred. No. 7.9e-20;
69; Mismatches 156;
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INTERLEUKIN-5 RECEPTOR.
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RESULT

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RESULT
10920K4
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Best Local
                                                                                                                                                                                                                                                                       Q9Z0K4;
                                                                                            Cavia porcellus (Guinea
Eukaryota, Metazoa, Chor
                                                                                                                                                                                           01-MAY-1999 (TrEMBLrel.
01-MAY-1999 (TrEMBLrel.
01-MAY-1999 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CHAIN SEQUENCE
     SEQUENCE FROM N.A. Norris T.E.;
                                                                                                                                                 GPIL-5RA.
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SIGNAL
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01-NOV-1996 (TYEMBLIE) 01, Last sequence up
01-NOV-1998 (TYEMBLIE) 08, Last annotation
INTERLEUKIN-5 RECEPTOR TYPE 2 PRECURSOR.
                                                                             Eutheria;
                                                                                                                                                                       INTERLEUKIN-5 RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE-PERIPHERAL BLOOD;
MURDLINE; 92121813.
MURATA Y. TAKAKI S., MIGITA M., KIKUCHI
"Molecular cloning and expression of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                   362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           136
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                363 LRKPNTYPKMIP 374
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                                                                                                                                                                                                                                                                                                                                                                                                                   CKICHLWIKLEP 373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EGT-RLSIQWEKPVSAFPIHCFDYEVKIHNTRNGYLQIEKLMTNAFISIIDDLSKYDVQV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LGRNIACWFPRTFILSKGRDWLAVLVNGSSKHSAIRPFDQLFALHAIDQINPPLNVTAEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -GONIGCREP--YLEASDYKDFYICVNGSSENKPIRSSYFTFQLQNIVKPLPPVYLTFTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      THITEDHYSRLRSYQVSLHCTWLYGIDAPEDIQYFLYYRYGSWIE-----ECQEYSKDI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DTEIKVNPPQDFEIVDPGYLGYLYLQWQPPLSLDHFKECTVEYELKYRNIGSETWKTIIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RAAVSSMCREAGLWSEWS-QPIYVGNDEHKP--LREW----FVIVIMATICFILLILSLI 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RSKVNIYCSDDGIWSEWSDKQCWEGEDLSKKTLLRFWLPFGFILIL-----VIFVTGLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -----YYNWQYLL-CSWKPGIGVLLDTNYNLFY----WYEGLDHALQCVDYIKAD 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ES --- KCVTILHKGFSASVRTILQ---NDHSLLASSWASAELH-APPGSPGTSIVNLTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KNLHYKDGFDLNKGIEAKIHTLLPWQCTNGSEVQSSWAETTYWISPQGIPETKVQDMDCV 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DEKISLLPPVNFTIKVTG-LAQVLLQWKPNPDQEQ-RNVNLEYQVKINAPKEDDYETRIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              p. Med. 175:341-351(1992).
x61177; CAA43484.1; -
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99; Conserv
                                                                           Rodentia;
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21
396 AA;
                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  . 20
396
44998
                                                                        iinea pig).
  Chordata; Craniata; Vertebrata;
  Hystricognathi; Cavidae; Cavia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14.8%;
                                                                                                                                                                       ALPHA
                                                                                                                                                                                           . 10, Created)
. 10, Last sequence 10, Last annotations.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 70;
                                                                                                                                                                                              Last sequence u
                                                                                                                                                                       PRECURSOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pred. No. 9e-
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 310.5; DB 4;
Pred. No. 9e-20;
D; Mismatches 156;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  POTENTIAL.
INTERLEUKIN-5 RECEPTOR TYPE
; 85FBF684 CRC32;
                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                             415
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on update)
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human interleukin
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                                                                                                 Mammalia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mammalia;
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.n 5
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SOLUTION OF THE PROPERTY OF TH
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Query Match 13.9
Best Local Similarity 28.0
Matches 89; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 14.2%;
Best Local Similarity 26.5%;
Matches 103; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                             Q15469 PRELIMINARY; rn., Q15469; Q15469; Q150469; Q1FEMBLrel. 01, Created) Q1-NOV-1996 (TIEMBLrel. 01, Last sequence update) Q1-NOV-1998 (TIEMBLrel. 08, Last annotation update) SOLUBLE INTERLEUKIN-5 RECEPTOR PRECURSOR.
                                                                                                      CHAIN
SEQUENCE
                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
TISSUE-PERIPHERAL BLOOD;
MUEDLINE; 92121815.
MURATA Y., TAKAKI S., MIGITA M., KIKUCHI
"MOLECULA" cloning and expression of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Cloning and Characterization of the Guinea Pi
receptor alpha cDNA.";
Submitted (APR-1996) to the EMBL/GenBank/DDBJ
EMBL; U55215; AAD09361.1;
                                                                                                                                               SIGNAL
                                                                                                                                                                                    J. Exp. Med. 175:341-351(
EMBL; X62156; CAA44081.1;
                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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SIGNAL 1
                                                                                                                                                                 Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                    Homo
                                                                                                                                                                                                                                receptor
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                                                                                                                                                                                                                                                                                                                                                                                                                  sapiens (Human).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ---WYEGLDHALQCVDYIKAD-GQNIGCRFP--YLEASDYKDFYICVNGSSENKPIRSSY 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AEH-KAPPGSPGTSIVNLTCTTNTAASNYTNLKSYEVSLHCTWLAGKDAPEDTQYFLYYR 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LAIGCLYTFLISTIFGCTSSSDTEIKVNPPQDFEIVDPGYLGYLYLQWQPPLSLDHFKEC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LPFGFILILVIFVTGLLLRKPNTYPKMIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TVENETYTLKTTNETRQLCFVVRSKVNIYCSDDGIWSEWSDKQCWEGEDLSKKTLLR-FW 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FTFQLQNIVKPLPPVYLTFTRESSCEIKLKWSIPLGPIPARCFDYEIEI-REDDTTLVTA 286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            YGPWTE-----ECQEYSKDTLSRNTACWFPRTFIHSKARDRLAVHVNGSSNHATIKPFD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TTYWISPQGIPETKVQDMDCV-----YYNWQ----YLLCSWKPGIGVLLDTNYNLFY- 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NLNYHVKINTPQEEDYE---TRNTQSKCETTLHQGVSASVRTIL-WH--GHSLLASSWVS 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TVEYELKYRNIGSETWKTIITKNLHYKDGFDLNKGIEAKIHTLLPWQCTNGSEVQSSWAE 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ILLGAIETLQTDTL-----PDKKFLLLPPINFTIKVTG-LAQVVLCWEPNPNQGQ-KNV 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TTTNA--FYSTTDGVSKYSIQVRAAVSPHCRAMGLWSKWS-QPVYVGKE--KKPIAGWFL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ITLTAVLCFILLIFFFLCRIYHLWTKMFP
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21
333 AA;
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                                                                                                                                                                                                          175:341-351(1992).
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333
37722
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                   13.9%;
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; Score 292; DB 4
; Pred. No. 3.1e-1
56; Mismatches 1
                                                                                                    POTENTIAL.
SOLUBLE INTERLEUKIN-5; E86A7792 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 298.5; DB 11
Pred. No. 1.1e-18;
7; Mismatches 172;
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O95646;
01-MAY-1999 (TrEMBLrel. 10, COL-MAY-1999 (TrEMBLrel. 10, IOL-MAY-1999 (TrEMBLrel. 10, INTERLEUKIN-)3 RECEPTOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Receptor.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
MORIMASA W., TERUMASA H.;
Submitted (DPC-1996) to the EMBL/GenBank/DDBJ
EMBL; U81379; AAD00510.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .192 -GQNIGCRFP--YLEASDYKDFYICVNGSSENKPIRSSYFTFQLQNIVKPLPPVYLTFTR
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                                                                                                                                                                                                                                                                                                                                                                                                                   52 WWPPEGAS--SNCSLWYFSHFGDKQDKKIAPETRRSI-----EVPLNERICLQVGS 100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    WOPPLSLDHEKECTVEY----ELKYRNIGSETWKTIITKNLHYKDGFDLNKGIEAKIHT 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LGRNIACWFPRTFILSKGRDWLAVLVNGSSKHSAIRPFDQLFALHAIDQINPPLNVTAEI
                                                                                                                                                               KPSENIVPLTSRVKPDPPHIKNLSFHND----DLYVQWENPQN-FYSRCLFYEVEVNNSQT
                                                                                                                                                                                                                                                                                                                                                       [J.FWQ: TNGSEVQSSWAETTYWIS-PQGIPETKVQDMDCVYYNWQYLLCSWKPGIGVLL 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DEKISLUPPVNETIKVTG-LAQVLL()WKENPDQEQ-RNVNLEYQVKINAPKEDDYETRIT
    WSNWSQEM----SIGKKRNSTLYITMLLIVPVIVAGAIIVLLLYLKRLKIIIFPPIPDP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RAAVSSMCREAGLWSEWS 326
                                                                                                                                                                                                        RSSYFTFQLQNIVKPLPP--VYLTFTRESSCEIKLKWSIPLGPIPARCFDYEIEIREDDT 281
                                                                                                                                                                                                                                                                                      DINENLEYWYEGIDHALQCVDYIKADGQNIGCRFPYLEASD - YKDFYICVNGSSENKPI 223
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KNIHYKDGFDLNKGIEAKIHTLLPWQCTNGSEVQSSWAETTYWISPQGIPETKVQDMDCV 146
                                         WSEWSDKQCWEGEDLSKKTLLREWLPE-----
                                                                               ETHNVFYVQEAKCENPEFERNVENTS---CFMVPGVLPDTLNTVRIRVKTNKLCYEDDKL
                                                                                                                        T-----LVTATVENETYTLKTTNETRQLCFVV------RSKVNIYC-SDDGI 321
                                                                                                                                                                                                                                                    DINYTLYYWHRSLEKIHOC-ENIFREGOYFGCSFDLTKVKDSSFROHSVQIMVKDNAGKI
                                                                                                                                                                                                                                                                                                                                 ----QCSTNESEKPSILVEKC--ISPPEGDPESAVTELQCIWHNLSYMKCSWLPGRNTSP
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Last sequence usualst annotation
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Pred. No. 4.7e-18;
9; Mismatches 139;
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annotation update)
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                                      -GFILILVIEVTGL--LLRKPNTYP 370
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097597;
01-MAY-1999
01-MAY-1999
01-MAY-1999
                                                                                                                          Q64146 PRELIMINARY: PRT; 896 AA. Q64146; Q1-NOV-1996 (TrEMBLrel. 01, Created) 01-NOV-1996 (TrEMBLrel. 01, Last sequence update) 01-NOV-1998 (TrEMBLrel. 08, Last annotation update) INTERLEUKIN-3 RECEPTOR BETA-SUBUNIT (FRAGMENT).
                            Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chor
Eutheria; Rodentia; Sciu
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea; Bovidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AF074402;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TRIGONA W.L., HIRANO A., BROWN W.C., ESTES D.M.;
"Biological activities of interleukin-13 on bovine lymphocytes:
implications for signaling through IL-13Ral.";
Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             )1-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-MAY-1999 (TrEMBLrel. 10, Last annotation update)
INTERLEUKIN-13 RECEPTOR ALPHA-1 CHAIN PRECURSOR (FR
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                                                                                                                                                                                                                                                                                                                                                                                                              NWS-----QAMSIGQKANQTFYIT--TLLIIPVIVAAAVI 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VPLTSHVKP-DPSHIKNLSFQNGDLYVQWTNPQN-FQSQCLCYEVEVINSHA--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          YYWHNSLGKILQCENFYR-EGQHIACSENLTKVKDSSFEQHSVQVMYRDNAGKISPSENI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EWSDKQCWEGEDLSKKTLLRFWLPFGFILILVIFVTGLLL 363
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FYWYEGIDHALQCVDYIKADGQNIGCRFPYLEASD--YKDFYICVNGSSENKPIRSSYFT 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CSTNESEKPS ILVEKCF-SPPEGDPESAVTALQCIWHNLRYMKCTWLPGRNASPDPNYIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WNPPEGAS -- PNCSLKY -- - FSHFGNKQDKKIAPET -HRSKEVPLNERICLQVGS -- -- Q 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WQPPLSLDHFKECTVEYELKYRNIGSETWKTIITKNLHYKDGFDLNKGIEAKIHTLLPWQ 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GKIFKEMFGD
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83; Conservative
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39644 MW;
                   Chordata; Craniata;
Sciurognathi; Murida
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 264.5; DB 6;
Pred. No. 9.1e-16;
53; Mismatches 135;
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                               Muridae;
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                         Vertebrata;
lae; Murinae;
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                            Rattus.
                                                      Mammalia;
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Best Local
CHEN J. GRACE A., CHIEN K.R.; Submitted (JAN-1998) to the EMEMBL; AF041845; AAAC03531.1; --
PFAM; PF00041; fn3; 4
SEQUENCE 881 AA; 99003 MW;
                                                                                                                                                                                                                                                                                                        Xenopus laevis (African clawed frog).
Eukaryota; Metazoa; Chordata; Craniata; Ve
Batrachia; Anura; Mesobatrachia; Pipoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-JUN-1998
01-MAY-1999
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                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                  XGP130
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            317 SDDGIWSEWSDKQCWEGEDLSKKTLLRFWLPFGFILILVIFVTGLLL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  155 CSWKPGIGVLLDTNYNLFYWYEGLDHALQCVDYIKADGQNIGCRFPYLEASDYKDFYICV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 204 LFLPNSIYVARVRAQLAPGSSLSGRPSGWSPEVHWDSPTE-DKARPQNLQCFFDGIQSLN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    107 TLLP------WQCTNGSEVQ---SSWAETTYWISPQGIPETKVQDMDCVYYNWQYLL
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896 896
896 AA; 99504 MW;
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Pred. No. 1.3e-07;
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           647E152E CRC32
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ea; Pipidae;
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354

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Query Match
Best Local S
Matches 88
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Best Local Similarity
Matches 75; Conserv
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01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-MAY-1999 (TrEMBLrel. 10, Last annotation update)
INTERLEUKIN-5 RECEPTOR BETA CHAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cavia porcellus (Guinea pig).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LOGSDON N.J., GRAHAM A., SCOTT C.W.;
"Guinea pig IL5 receptor beta chain.";
"Guinea (MAR-1997) to the EMBL/GenBank/DDBJ
EMBL: U94688; AAC77520.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q9Z1A0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         223
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          34 PPQDFEIVDPGYLGYLYLQWQPPLSLDH----FKECTVEYELKYRNIGSETWKTIITKNLH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EYELKYRNIGSETWKTIITKNLHYKDGFDLNKGIEAKIHTLLPWQCTNGSEVQSSWAETT 127
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QYEILNQTTSSVTFENLTTLN-----SPLTCNVMASGHV----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                YTLK-----TTNETRQLCFVVRSKVNIYCSDDGIWSEWSD--KQCW-----EGEDLSKK 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ELISSLELPNALKIEWKNPITNAFNLKYNIRYRPVKTQDWEM-VPEEDT-----ASHRDS
                                                                                                         KLKWSIPLGPIPARCF-----DYEIEIREDDTTLVTATVENETYTLK------
                                                                                                                                                                                                                                                                                                                                                                                      VQDMDCVYYNWQYLLCSWKPGIGVLLLTNYNLFYWYEGLDHALQ-CVDYIKADGQNI---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SNSSQAALGPELFLPSSTYVARVRTRL----ARGSGFSGRPSQWSPEVSWSSQPG-DQAQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PPQDVQINTSG--DQVLLTWSVALEGPHTSWLSQRDLEFEVVYKRL-HEPWESAST--LH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ----CRGANNSCTIHSPGFQFYIDTTFQVEATNELGIQKSETLTIDPVNIVKPNPPQLS 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VDYIKADGONIGCRE PYLEASDYKDEYICVNGSSENKPIRSSYFTFQLQNIVKPLPPVY- 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  YGIFFTLGLPPDKPTNLTCIVYNQDNLTCTWDPGRPTNLPTNYTLSHRWAHFGANY----
                                                                                                                                                                                  HSCQIRVSNPRPHSQYTVTVRPRNGEKFIRSA-----NHIQMAAPT-LNVTKDGD-TY
                                                                                                                                                                                                                                                   -GCRFPYLEASDYKDFYICVNGSSENKPIRSSYFTFQLQNIVKPLPPVYLTFTRESSCEI
                                                                                                                                                                                                                                                                                                                            PQNLQCVFDGAHTLSCSWEVRSQVTSSVSFGLFY-RSSLDAGEQECPQVQKEELHDIYTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -----FDLNKGIEAKIHTLLPWQCTNGSEVQ---SSWAETTYWISPQGIPETK 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  890 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative .
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                                       VTEKMYYSHIENTFEIQYR---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8.28;
25.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      96579 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8.1%; Score 170; DB 11;
23.8%; Pred. No. 6.8e-07;
Live 53; Mismatches 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Score 173.5; DB 13;
; Pred. No. 3.3e-07;
37; Mismatches 115;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EABC43CC CRC32;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 890;
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                      046561 PRELIMINARY;
046561;
01-JUN-1992 (Trembirel 06, Cr
01-JUN-1998 (Trembirel 06, Las
01-MAY-1999 (Trembirel 10, Las
PROLACTIN RECEPTOR LONG FORM P
                                                                                                                                                                                                                                                                                Ovis aries (Sheep):
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Cetartiodactyla; Ruminantia; Pecora; Rovo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bos taurus (Bovine).
Sukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Surheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea; Bovi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-JAN-1998 (TIEMBLIEL 05, Created)
01-JAN-1998 (TIEMBLIEL 05, Last sequence update)
01-JAN-1998 (TIEMBLIEL 08, Last annotation update)
PROJACTIN RECEPTOR SHORT FORM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         018880;
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                                                                        SFCTENCE FROM N.A.
MEDLINE; 98001468.
BIGNON C., BINART N.,
SJITAKE J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Endocrinology 138:3187-3194(1997).
EMBL; AF027403; AAB83999.1; -
PFAM; PF00041; fn3; 2.
SEQUENCE 296 AA; 33854 MW; 8B40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE; 97375450.
SCHULER L.A., MAGEL R.J., GAO J.,
"Prolactin receptor heterogeneity
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       s of the ovine prolactin receptor: cDNA cloning reveal that the two forms arise by different
                                                                                                            ORMANDY C.,
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                                                                                                                SCHULER L.A., KELLY P.A.,
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Mustela vison (American mink).

Mustela vison (American mink).

Finkaryota; Metazoa; Chordata; Craniata; Vertebrata; Merican mink).

Finkaryota; Metazoa; Chordata; Mustelidae; Mustela
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Submitted (JAN-1998) to the
EMBL; AF041257; AAB96795.1;
PFAM; PF00041; fn3; 2.
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                                                                                                                                                                                                                                                                                                                                                                                                      DUDE A., MURPHY B.D.;
EMBL/GenBank/DDBJ databases
                                                                                                                                                                Score 153; DB 6;
Pred. No. 3.7e-06;
86; Mismatches 87
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299665;
01-MAY-1997 (TremBirel. 03, C
11-MAY-1997 (TremBirel. 03, I
01-NOV-1998 (TremBirel. 08, I
                                                                                                                Q16354 PRELIMINARY; PRT; 206 AA. 016354; U1-NOV-1996 (TrEMBLrel. 01, Created) 01-NOV-1996 (TrEMBLrel. 01, Last sequence update) 01-NOV-1998 (TrEMBLrel. 08, Last annotation update) PROLACTIN RECEPTOR (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.

PRESKY D.H., YANG H., MINETTI L.J., CHUA A.O.,
GATELY M.K., GUBLER U.;
Submitted (JUL-1996) to the EMBL/GenBank/DDBJ
EMBL; U64198; AAB36675.1;
PFAM; PF00041; fn3; 3.

SEQUENCE 862 AA; 97134 MW; SFE4FBD5 CRC32;
                                                                Homo sapiens (Human)
Eukaryota; Metazoa;
                                   Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eutheria; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IL-12 RECEPTOR BETA2.
                                                                                                                                                                                                                                                                                                                                                                                                                                           339 QQISLFW 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        339 KTLLREW 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     282 LDLKPFYEYEFQISSKLHLY----KGSWSDWSESLRAQTPEEEPTGMLDVWYMKRHIDYSR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           87 KNLHYKDGFDLNKGIEAKIHTLLP--------WQCTNGSEVQSSWAETTYWISPQGIPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    59 NEMGSSSSDP---RYVT--LTYIVEPDPPVNL---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TFTRESSCEIKLKW------SIPLGPIPARCFDYEIEIREDDTTLVTATVENETYTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KPDHGFWSEWSPKRSIQIPNDISMKDTI-VWI---FVAVLSAVICLIMVAAVALK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KFQKASVSRCTLYWRDEGLVLLNRLRYRPSNSRLWN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADGQNIGCRF-PYLEASDYKDFYICVN--GSSENKPIRSSYFTFQLQNIVKPLPP--VYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TKYQDMDCYYYNWQ-YLLCSWKPGIGYLLDTNYNL-----FYWYEGLDHALQCYDYIK 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RRINFHHGHSLNSQV-----TGLPLGTTLFVCKLACINSDEIQICGAEIFVGVAPE---- 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                S-DDGIWSEWSDKQCWE-GEDLSKKTLLRFWLPFGFILIL----VIFVTGLLLR 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TLVDVRSGWLTLQYEIRLKPEKAT----EWETHFAGLQTQFKILSLYPGQKYLVQVRC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KTTNETRQLCFVVRSKVNIYCSDDGIWSEWSDK---QCWEGE------DLSK 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CDYLDFGINLTPESPESNFTAKVTAVNSLGSSSSSLP---STFTF--LDIVRPLPPWDIRI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -QPQNLSCIQKGEQGTVACTWERGRDTHLYTEYTLQLSGPKNLTWQK-----QCKD-IY 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GPIPAR----CFDYEIEIREDDTTLVTATVENETYTLKTTNETRQLCFVVRSK--VNIYC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                   Catarrhini;
                                                         Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 151;
Pred. No. 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Last sequence update)
                                                                   Craniata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                   Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hominidae; Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CHUA A.O., NABAVI N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     862
                                                                   Vertebrata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 4;
.2e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ---SLELKOPEDKKTYLWIKW-YPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     À
                                   Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                   Mammalia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C.Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   232
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Best Local Similarity 27.9
Matches 58; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cancer cell lin
J. Biol. Chem.
EMBL; S78505; A
PFAM; PF00041;
NON_TER 1
SEQUENCE 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A
MEDLINE; 95286597
FUH G., WELLS J.A
168 KILSLHPGQKYLVQVRCKPDHGYWSAWS 195
                                302 RQLCFVVRSK--VNIYCS-DDGIWSEWS 326
                                                                                                                                255 K-----LKWSIP-LGPIPARCFD--YEIEIREDDTTLVTATVENETYTLKTTNET 301
                                                                                                                                                                                                                                                                                                            135 IPETKVQDMDCVYYNWQYLLCSWKPGIGVLLDTNYNLFYWYEGLDHALQCVDYIKADGQN 194
                                                                                       114 KOPEDRKPYLWIKWSPPTLIDLKTGWFTLLYEIRLKPE-----KAAEWEIHFAGQQTEF 167
                                                                                                                                                                                                                            195 IGCRFPYLEASDYKDFYICVNGSSENKPIRSSYFTFQLQNIVKPLPPVYLTFTRESSCEI 254
                                                                                                                                                                61 -SCHFGKQYTSMWRTYIMMVNATNQMGSSFSDELYVDVTYIVQPDPPL-----ELAVEV 113
                                                                                                                                                                                                                                                                       2 LPPGKPEIFKCRSPNKETFTCWWRPGTDGGLPTNYSLTYHREGETLMHECPDYI-TGGPN 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      206 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      . 270:13133-13137(1995).
AAB34470.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      entagonists that inhibit the growth of breast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23950 MW; L.7E57266 CRC32;
                                                                                                                                                                                                                                                                                                                                                        7.2%; Score 151; DB 4; Length 206; 27.9%; Pred. No. 5.2e-06; tive 26; Mismatches 94; Indels
                                                                                                                                                                                                                                                                                                                                                          30; Gaps
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Search completed: January 20, 2000, 06:37:46 Job time: 1004 sec

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